

0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99

[illegible]

## FIGURE 2

MTDSPPPGHPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTQCSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSADGTLCPVKGFPFPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS

### **Signal sequence:**

amino acids 1-19

### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

### **N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

### **Amidation site.**

amino acids 26-30

### **Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

### **Cell attachment sequence.**

amino acids 130-133

### **EGF-like domain cysteine pattern signature.**

amino acids 123-135

# FIGURE 3

CGCTCGCCCCGTCGCCCCCTCGCCTCCCCGAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG  
 GTCAGCCCCAGCGGGGGGACTATGGTGAAATTCCCGGCGCTCACGCACTACTGGCCCCGTGATC  
 CGGTTCTTGGTGCCCCCTGGGCATCACCACATAGCCATCGACTTCGGGGAGCAGGCCCTTGAA  
 CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGGCTGGCGT  
 ACTCCCTCATGAAGTTCTTTCACGGGTCCCATGAGTGACTTCAAAAAATGTGGGCTGGTGTTT  
 GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCTGTGTATGGTGGTGCGCAGGGGCCCATCGC  
 TGCCGTCTTTTACACACATGATAGCTTATAGTGATTAGGATACTACATTATCAATAAATGCG  
 ACCATTGTGACGAGTCCGTTGGGGAGCAAGACGAGAAGGGCTTCTGTACTCTCGCCGCTTT  
 CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAAAACAAAAACAGTTT  
 CCTGGTGGGATGTGCCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTGTAGCCATTTTGC  
 TTCACAGTCACTGGAATGCCGGGAGCCCCCTGCTCATCCCCGATCTCTCCTTGTACATGGGC  
 GCACCTGTGCGCTGCACCACCCTGTGCCCTGGGCTACTACAAGAACATTACGACATCATCCC  
 TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
 GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT  
 TCCCTGGGACCTTGTGGCGAGTTCTGCAGCCACAGAGGCAGTGGCGATTGTGACAGCCACATA  
 CCTCTGGGTGATGATGCCATACGGCTGGTTGACGGAATCTCGTGTGTGATCTCTGCTTTTCG  
 ACAAGAATAACCCAGCAACAAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCACATC  
 AAGAAGTTCACTTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTCGTGATGTTTGGAGAC  
 ACCCAACGTGTCTGAGAAAACTTGTATAGACATCATCGAGTGGAATTTGCTTTTGCAAGC  
 TCTGTGTTGTTCTCTTTCGGGATCTTCTCTCTTCTCCAGTTCCAGTCAAGTGAGGGCGCAT  
 CTCACGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGGCCCCAGCTCTGTGCTCGG  
 GATCATCTGCTCATCGCCAGCTCGTGGTCTTACCCTACCTGGGGTGCACGGTGCGGACCC  
 TGGGCTGGGCTCCCTCTTGGCGGCTTGTGGGAGAATCCACCATGGTCGCCATCGCTGGG  
 TGCTATGTCTACCGGAAGCAAAAAGAAAGATGGAGAATGAGTCGGCCACGAGGGGGAAGA  
 CTCTGCCATGACAGACATGCCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG  
 AGAATGAATAAGGACACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC  
 GGCATCATCTCTTCCCCTCTCCCATCGTATTTTGTCTCCCTTTTTTTGTTTTGTTTTGGTAAT  
 GAAAGAGGCTTGAATTAAGGTTTCGTGTCAATTCTCTAGCATATCGGATGATGCTCACACT  
 GACGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAACGAAACAACCTGAC  
 TTCATACCCCTGCCCTCACGAAAACCCAAAAGACACAGCTGCCCTACGGTTGACGTTGTGTCC  
 TCCTCCCCCTGGACAATCTCCTCTTGAACCAAAGGACTGCAGCTGTGCCATCGCGCTCCGTT  
 CACCTCTGCACAGCAGGCCACAGACTCTCTGTGCCCTTCTATCGCTCTTAAGAAATCAACAGG  
 TTAAACTCGGCTTCTTTGATTGCTTCCAGTCACATGGCCGTACAAAGAGATGGAGCCC  
 CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATTCTACTCCACACATGCAG  
 GAGGCGGGTGGCACGCTGCAGCCCGGAGTCCCGGTTACACTGAGGAACGGAGACCTGTGAC  
 CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAATGCCCCGGG  
 GGCAGCAACTGACATGGTTGAATGATAGCATTTCACTCTCGCTTCTCTAGATCTGAGCAA  
 GCTGTGACTTCTCACCCCCACCGTGTATATACATGAGCTAATCTTTTAAATTTGTACAAAA  
 GCGCATCTCCAGATTCCAGACCCTGCCGATGACTTTTCTGAAGGCTTGCTTTTCCCTCGC  
 CTTTCTGAAGGTCGATTAGAGCGAGTCACATGGAGCATCTCACTTTGCAATTTTAGTTTTT  
 TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATTCTAATGCCAGGTTGCTGTAGGGTAAC  
 TTTTGAAGTAGATATATTTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTA  
 TTGAGAAATGTACTACGGTACTTCCCTCCACACCATACGATAAAGCAAGACATTTTATAACG  
 ATACACAGATCAGTATGTGGTCTCCCTGAAATAACGCATTGCAAAATCATGAGTGCAGTA  
 TATTTTTCTAAGTTTGGAAAGCAGGTTTTTCTTAAAAAAATATAGACACGGTTTCACT  
 AAATTGATTTTAGTCAGAAATCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA  
 TAAATATATGCTGTATATGTTATGTAATTTATTTAGGCTATAATACATTTCTCTATTTTCG  
 ATTTTCAATAAAATGTCTCTAATACAAAAA

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## **FIGURE 4**

MVKFPALHYWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSDFKNVGLVFNNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSIDLGYIINKLHHVDESV  
GSKTRRAFLYLAAFPFMDAMAWTHAGILKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC  
REPLLLIPILSLYMGALVRCTTLCGLGYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL  
ATQORISRPVNLVFSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN  
KLVSTSNVTAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLR  
IFSFFPVPTVRAHLTGWLMTLKKTFVLAPSSVLRIRVLIASLVVLPYLGVBHATLGVGSL  
AGFVGESTMVAIAACYVYRKQKKMENESATEGEDSAMTDMPTTEEVDIVEMREENE

### **Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

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## FIGURE 5

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG  
ACAAGAATAACCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTGGAC  
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCCAGTTCACAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC

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## **FIGURE 6**

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGCAAAACAGTNACGGGCAGCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT  
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTCCITTTGCGGATTTTCT  
CCTTTTCCCAGTTCCAGTCACAGNGAGGGCGCATCTCACC GGNGGNTGATGACANTGAAG  
AAAACCTTGTCTCTGCCCCAGCTNNTTGGTGCGGATCATTGTCCTNATNGCCAGCCTTGT  
GGTCCTACCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCCTCCTGGCGGGCA

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## FIGURE 7

TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTACCGGGTGGCTGANGAACTGAAGAAA  
ACCTTNGTCCTTGCCCCAGNTTTGTGNTGCGGAINATCGTCCTCATCGCCAGCCTNGTGGT  
CCTACCCTACCTGGGGGTGCACGGTGAGAC

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# FIGURE 8

GCCCCGCGCCCCGGCGCCGGGCGCCCCGAAGCCGGGAGCCACCGCCATGGGGGCTGCCTGGGA  
 GCCTGCTCCCTGCTCAGCTGCGCGTCTGCCTCTGCGGCTCTGCCCTGCATCCTGTGCAG  
 CTGCTGCCCCGCCAGCCGCAACTCCACCGTAGCCGCTCATCTTACAGTTCTTCTCTTCC  
 TGGGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGCGTGGAGAGTCAGCTCTACAAGCTG  
 CCCTGGGTGTGTGAGGAGGGGGCGGGATCCCCACCGTCTGACGGGCCACATCGACTGTGG  
 CTCCTGCTTGGCTACCGCGTGTCTACCGCATGTGCTTCGCCACGGCGGCTTCTTCTTCT  
 TCTTTTTCACCTGTCTATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
 AATGGGTTTTGGTTCTTTAAGTTCTTGATCCTGGTGGGCTCACCGTGGGTGCCTTCTACAT  
 CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCTGGGCTCCTTCCTCTTCA  
 TCCTCATCCAGCTGGTGTGCTCATCGACTTTGCGCACTCTGGAACCAGCGGTGGCTGGGC  
 AAGGCCGAGGAGTGCATTCCCGTGCTGGTACGCAGGCTCTTCTTCTTCACTCTCCTCTT  
 CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTATGTAATACTGAGCCAGCGCT  
 GCCACGAGGGCAAGTCTTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
 GCTGTCTCGCCCAAGGTCCAGGACGCCAGCCCAACTCGGGTCTGCTGCAGGCCCTCGGTCTAT  
 CACCCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCTGAACAGAAATGCA  
 ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
 ACCCAGTGGTGGGATGCCCGAGCATTGTGGGCTCATCATCTTCTCCTGTGCACCCTCTT  
 CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
 CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGCCCGGGCC  
 TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGTCT  
 GGCTCACTGCACGTATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
 TGATCAGCACGTGGACCCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
 TACCTGTGGACCTGGTAGCCCCACTCCTCCTGCGCAACCGCACTTCAGCTGAGGAGCCT  
 CACAGCCTGCCATCTGGTGCTCCTGCCACCTGGTGCCCTCTCGGCTCGGTGACAGCCAACCT  
 GCCCCCTCCCCACCAATCAGCCAGGCTGAGCCCCACCCCTGCCCCAGCTCCAGGACCTG  
 CCCTGAGCCGGGCTTCTAGTCGTAGTGCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
 GAGCCCCATCCCCCGCCACACCCACAGGTGGAGTGCCTTCTTCTTCCCTCCTCCTGT  
 TGCCCATACTCAGCATCTCGGATGAAAGGGTCCCTTGTCTCAGGCTCCACGGGAGCGGGG  
 CTGCTGGAGAGAGCGGGAACTCCACCAAGTGGGGCATCCGCACTGAAGCCCTGGTGT  
 CCTGGTCACGTCCCCAGGGGACCTGCCCTTCTTGGACTTCGTGCCTTACTGAGTCTCT  
 AAGACTTTTCTAATAAACAGCCAGTGCCTGTAAAAAAA

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## **FIGURE 9**

MGACLGACSLLSASCCLCGSAPCILCSCCPASRNSTVSRLIITFFLFLGVLVSIIMLSPGVE  
SQLYKLPWVCEEGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSFLFILIQLVLLIDFAHSW  
NQRWLGAEECDRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCGHEGKVFISLNLTFC  
VCVSIAAVLPKVQDAQPNSSGLLQASVITLYTMFVTWSALSSIPEQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA  
ACEGRAFDNEQDGVITYSYSFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVVVKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

### **Signal sequence:**

amino acids 1-20

### **Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

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## FIGURE 10

GAGCGAGGCCGGGGACTGAAGGTGTGGGTCTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCGAGTCTTTGCTGCCGAAGCTG  
TGACTGCCGATTCCGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGTGCCACACGAGGCTT  
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAAATTGCAGGA  
GCTGTACCGGAAGTCTTTTATAGGATAAACGTAGGCCTGCGTGCCCTGGTGGCTGGTGGCAT  
AATTGAGCCTTGCTGGGCACTCCTGTAGGAGGCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTTTTCAGGAAAGAAAACAGAAGGATCGAAAGGCATCCATGAGCTAAAACCTGGAA  
GAGTGGAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAAAC  
CTTCAGTAATAGATAAAACAAGACAAGGACTTGAAAGTGCTCTGAACTTGAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCTTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTCTTTCTTT  
TTTAACTAAGAAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAACATTTTCGAAAAGATTAAAGTTGAATTTTACAGTTT

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[illegible]

### Important Features:

amino acids 1-24

amino acids 76-96 and 171-195

## amino acids 153-156

## **FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTGTTTCATG  
GCTGGCGCCGAACC

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# FIGURE 13

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCGAGTTTTTGTCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGAATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAAGCTTTTATTTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

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[illegible]

GAGCCGCGCCGCGCGCGCGCGCCGCGCACTGCAGCCCCAGGCCCCGGCCCCCACCACGCTCT  
GCGTTGCTGCCCCGCGCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCAAGGGAACT  
CCGCCGAGTTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGCGTTGCGGG  
GCTTCGCGTGTCTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGTTAGTCTG  
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT  
CGGCGTGTGTCATTGCAGTGGGCATCTTCTTGTTCTGATTGCTTTAGTGGGTCTGATTGGAG  
CTGTAAAAACATCATCAGGTGTGCTATTTTTTTATATGATTATTCTGTTACTTGTATTATT  
GTTTCAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT  
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT  
GTGGGTTCCGAAGTGTTAAACCCAAATGACACCTGTCTGGCTAGCTGTGTTAAAGTGACCAC  
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTGG  
TGGCATTTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGCTGACCTACAGATAA  
GGAACCGAAGACCCCGCGCAATCTAGTGCATGCTGTTGATGAGAAACCAAGSAGAT  
TTCCTTTGCTATTATGCTGCTTGTTCACCTTTCTGTAATTTCTGTTAAAGCTCCATTGTCCAGT  
TTAAGGAAGGAACACACTATCTCGAAAAGTACCTTATTGATAGTGAATATATATTTTTACT  
CTATGTTTCTCTACATGTTTTTTCTTTCCGTTGCTGAAAAATATTGAAACTGTGGTCTC  
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCTATTGTCGGGCACGTGCCACTGTGGCCTT  
TCTTAGCATTTTTACCTGCAGAAAAACTTTGTATGGTACCACTGTGTTGGTTATATGGTGAA  
TCTGAACGTACATCTCACTGGTATAAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC  
TGGAAGAAAGAGTGGAATTTATTAAGTATGAGATCCTGTTATGTTAAGGGAAA  
TCCAAATCCCAATTTTTTTTGGTCTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA  
TAAAAATGATAATTACTTGTAGTCTTTATGATTACACCAATGATATTCTAGAAATAGTTAT  
GTCTTAGGAAATGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAGAGGAGAAAGTGTTT  
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT  
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAAATTGAAAGTCTAA  
AAGACTGCATTTTTAAACAAGTTAGTATTAAATGCGTTGGCCACGTAGCAAAAAGATATTTG  
ATTATCTTAAAAAATGTGTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAAACAGCAACTT  
GTCAAACCTAAGCATGTTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATTGTGTG  
GCTCTGTATATTCTGTTAAAAAATTAAGGACAGAAACCTTCTTTGTGTATGCATGTTTGA  
ATTAAAGAAAGTAATGGAAG

## **FIGURE 15**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVIIVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLVFIQFSVSCACLALNQEQQGQLLEVGNWNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRFRVGGIGLFFSFTEILGVWL  
TYRYRNQKDPANPSAFL

### **Signal Peptide:**

amino acids 1-34

### **Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

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## **FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCCGAAGTGTTAACCCAAATGACACCTGTNTGGCTAGCTGTGTTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

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## FIGURE 17

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTAAACAAGTTAGTATTAATGCCTTGCCCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCATAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

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## FIGURE 18

ATGATTATTCTGTTACTTGTATTTATTGTTTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTAAACC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

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# FIGURE 19

CAGTCACCATGAAGCTGGGCTGTGTCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
 CTCTGGGTGGCCACAGATGCTACTGGCTGCCAGTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
 CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTTGATGCAAGGGGAAGCTGGCT  
 TCCAGGTCAAGGCCTACACTTTCACTGAACCTTCCACCTGATTGTGTCTTATGACTGGCTG  
 ATCTCCAAGGTCCAGCCAAAGCCAGTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
 CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
 CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
 TGCAGTGGCATCTTCCAGAGCCCTGGTCTCTGGGATCCAGAAACAGCATCTGTTTGTGGCTAT  
 CACAGTCCAAGAACTGTTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
 CAGGAAGCCCCATGACCTCAGTTGTGAGACAAAGTTGCCCTGCAGAGGTCAGCTGCCCGC  
 CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
 CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCTACTGGTGTGAGGCAGCCACTGAGG  
 ACAACCAAGTTTGGAACACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
 GCTGCACCTCCCACTTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAATGCTCCTGA  
 GGAGGCCCTGGGCCTCTGCCTCCGCCCAACCCCATCTTCTGAGGATCCAGGCTTTTTCTT  
 CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACAGATGGGCTTTCTTCAAAACACATG  
 CAGGATGTGAGAGTCTCTCTCGGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
 GAAGCCTGGGACCACAAGGCTACTGCTGAATAGAAAGTAAACAGTTTCATCCATGATCTCACT  
 TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTCTCTGCTGCAATATGCATAAGTA  
 CTTTTACAAGTTGTCCAGTGTTTTGTGAGAATAATGTAGTTAGGTGAGTGTAAATAAATTT  
 ATATAAAGTGAGAATTAGAGTTTAGCTATAATGTGTATTCTCTCTTAACACAACAGAATTC  
 TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
 CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGCAATTTTCCCCCAGAGGACA  
 TTGGGCAATGTTTGAGACATTTTGGTCATTATACCTTGGGGGTTGGGGATGGTGGGATGT  
 GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG  
 GGCAGTACCCCAACAAAGAAATAATCTGGCCCAAATGTCAAGTTGTACTGAGTTTGAGAAA  
 CCCCAGCCATGAACCCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
 TATCTCTTCCAGCCTCATTGAGCTATTCTTACTGACATACCAGTCTTTAGCTGGTGCTATG  
 GTCTGTTCTTTAGTTCTAGTTTGTATCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
 AAGGTGATGGCATTAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
 ATGATTAGGATTAGTGCCCTTATTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
 ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCAAAAAACAGCTGTGCCCAACACCG  
 ACTCTGTCGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATCTGG  
 TTGTTGTAGCCATA

0976192-101501

## FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594  
><subunit 1 of 1, 359 aa, 1 stop  
><MW: 38899, pI: 5.21, NX(S/T): 0  
MKLGCVLMAWALYLSGLVWVAQMLLAASFETLQCEGPVCTEESCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAPVFEGDLLVLRCAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWQSQPQLEIRVQGASSAAPTINPAPQKSAAPGTAPEEAPGPLPPPPTPSSSDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

### Signal sequence:

amino acids 1-17

### Leucine zipper pattern sequence:

amino acids 12-33

### Protein kinase C phosphorylation site:

amino acids 353-355

0957353-355

## FIGURE 21

CCCACGCGTCCGCCACGCGTCCGCCACGGGTCGCCACGCGTCCGGGCCACCAGAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
ATCTTACTGGGCTGTACTCTCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
GGAAGTGCCAGAGAGTGTAAACAGGACCTTGAAAGGGGATGTGAATCTTCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAAGTACAGGGCCG  
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCCTGGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCTGT  
AGAGATAAGATTACTGAGCTCCGTTCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTACGCGTCCCCAGGGAATGAGGATTAGCCCTCAATGCCAGGCTC  
GGGGTTCTCCTCCCATCAGTTATATTTGGTATAAGCAACAGACTAATAACCAAGGAACCCATC  
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCACTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGGCCATCATCCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTTACCATGGCCTATATCATGCTCTGTGCGAAGACATCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTCCATTTTTGACCCCGT  
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC  
AATCTAAGGCCGGAGGCCCTTCAAGGTGAGGACATAGCTGCCCTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAAGGTTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGAGAAACCATGAGGGTGCCCATCTTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACTTCCAGAACTTGGGCAACAACTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCCGCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAAGTGTCTGTTAAAAATGCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCCTTCTGCAATGGCCTTCTCCCTGCT  
ACCTCTCTTCCCTGGATAGCCAAAGTGTCCGCCTACCAACACTGGAGCCGTGGGAGTCACT  
GGCTTTGCCCTGGAATTGGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTGGCTCTGG  
GCCCTTCTAGTATCTCTGCCGGGGCTTCTGGTACTCCTCTCTAAATACCAGAGGGAAGATG  
CCCATAGCATAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTTCTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTTCAGGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

09978392-101501

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLLGHLLTVDTYGRPILEVPESVTGPNKGDVNLPCITYDPLQGYTQVLVKWLVQRGS  
DPVTIFLDRSSGDHIQQAKYQGRILHVSHKVPDVSLLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRIQLQCQARGSPPISYIWKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT  
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAILLIISLCCMVVFTMAYIMLCRKT  
SQQEHVYBAAR

### **Signal Sequence:**

amino acids 1-19

### **Glycosaminoglycan attachment site:**

amino acids 149-152

### **Transmembrane domain:**

amino acids 282-300

03976192.101501

# FIGURE 23

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGCGCGCTCCGCCCCGCACAT  
 GGCTGCAGCCACTCGCGCGCACCCGAGGGCGCGCGCCAGCTCGCCCCAGGTCGCGTCGGA  
 GCGCGCCGCGCGCCCCGGGAGCCAAAGCAGCAACTGAGCGGGGAAGCGCCCGCTCCGGGGATC  
 GGGATGTCCTCTCTCTTCTCCTCTTGCTAGTTTCTACTATGTGTGGAACCTTGGGGACTCA  
 CACTGAGATCAAGAGAGTGGCAGAGGAAAAGTCACTTTGCCCTGCCACCATCAACTGGGGC  
 TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
 GTGGTGATCACTTACTCCAGTCGTATGTCTACAATAACTTGACTGAGGAACAGAGGGGCGC  
 AGTGGCCTTTGCTTCCAATTTCTGGCAGGAGATGCCTCCTTGACAGATTGAACCTCTGAAGC  
 CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTGAGGGCGCTACGTGTGGAGCCAT  
 GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAGGTGTGAGTTTGAAGGAGAGCTGAC  
 AGAAGGAAGTGACCTGACTTTGCACTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT  
 ACTGGCAGCGAATCCGAGAGAAAAGGGAGAGGATGAACGTCTGCCTCCCAATCTAGGATT  
 GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCTACTCTGGAGTGA  
 CCAGTGCCACAGCAGGCAACGAAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACGTACAGT  
 ATGTACAAGCATCGGCATGTTGTCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
 ATTTTCTCCTTTGGTGTGGCTGCTAATCCGAAGGAAGACAAAGAAAGATATGAGGAAGAAGA  
 GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCCTCTTGTGAAACCCAGCT  
 CCTCTTCTCAGGCTCTCGGAGCTCAGCTCTTGGTCTTCTCCTCACTCGCTCCACAGCAAT  
 AGTGCTCTCAGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCAGCCAGGGCTGGCCAC  
 CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCTAG  
 CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCTCTCAA  
 ACGGTCGTAATTACAATGGACTTGACTCCCACGCTTTCTAGGAGTCAGGGCTTTTGGACTC  
 TTCTCGTCAATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCACTAAGTAGCA  
 GTGAGCAATTGCAGGAACAGATTGAGATGAGCATTTTCTTATACAATACCAAACAGCAAA  
 AGGATGTAAGCTGATTCACTGTAAAAAGGCATCTTATTGTGCCCTTAGACCAGAGTAAGGG  
 AAAGCAGGAGTCCAAATCTATTGTGTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
 AGGTGAATATACCTAAAACCTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT  
 TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTCTATGCATTTCTGCAAACTATTGGATT  
 ATTAGTTATTGACAGCTCAAGCAGAACCCAGCCCTATTATCACTGTCTACACCATGTAC  
 TGAGCTAACCCTTCTAAGAAACTCCAAAAAGGAACATGTGTCTTCTATTCTGACTTAAC  
 TTCATTGTGCATAAGGTTTGGATATTAAATTCAGGGGAGTTGAAATAGTGGGAGATGGAGA  
 AGAGTGAATGAGTTCTCCCACTCTATACTAATCTCACTATTGTGATTGAGCCCAAAATAAC  
 TATGAAAGGAGACAAAATTTGTGACAAAGGATTGTGAAGAGCTTCCATCTTCATGATGTT  
 ATGAGGATTGTTGACAAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCTTCAAA  
 CAGATGCTCTAAGGACTTTCTCTGCTAGATATTCTGGAAGGAGAAAAATACAACATGTCTATT  
 TATCAACGCTCTTAGAAGAAATTTCTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATT  
 CCAACATCACTTATAGTCTCTTCTTCTGAGAAAATGTGAAACCAAGAAATTGCAAGACTGG  
 GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
 TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTGCAAGTGAGCCGAGATTATGCC  
 ATTGCATCCAGCTGGGTGACAGAGCGGACTCCGCTCTC

00978152.401501

## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTLCCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPQSRAFQTV

### **Signal sequence:**

amino acids 1-16

### **Transmembrane domain:**

amino acids 232-251

09078192-101501



## 0697876203

TGTGTTCTCTTTGCTGCTCTCTGCGCCAGTCTCTCTCTCTGGTCTCTCTCAGCCGCTGTGCGGAGGAGAGACAACCGGAG  
 CAGCCGGGCTCAGCTCTCGGGCGGCTCTCTCCGGCTCGGGCGGCGGCTCGCCGCTGGGAGAGGTCTGAGCGCCCTAG  
 AGCCTCTCTGCTTGCAGCTCTCCCTCTCTCTGCCCGGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG  
 GCCCGGGGAGGGCGCGGTGGATGCGCGCTGGGAGCAGGACAGCGCCGATTTCCAGCTGCCCGCGCGCGCCCGGGG  
 CCCCCTGCGAGTCCCGGTTTCAGCCATGGGGGACCTCTCCGAGCAGCAGCAGCCGCTCTGCGATCTCTGCGACGCGCAT  
 GCCCGCGGAGCCAGCAGCCAGCATGATGCGGGGCTCCCTTCTCTGCTTGGATCTCTTAGCACCCACACAGCTCAG  
 CAGAAAGAGAGGCGCTCGAATCTCATTTGGCACAATACGCCATGTGAACCGTGCCACACCGGCGAGGTGCTAACCCTGT  
 GACAAGTGTCCAGCAGGAACCTTATGTCTTGAGCATTTGACCAACCAAGCGCTGCGGCTCTGCGAGCATTTGCCCT  
 GTGGGAGCTTTTACAGGACATGAGATGGCATGAGAAATGCGATCATGTAGTACGCCATCTGAGCATTTGCCCAAT  
 ATTAGAGAAATTTACTTGTGCTGCTTGATGACGAGAGATGCATCTGCCCACTGGCATCTGTTCAGCTCTTAAGCGT  
 AACTGTGCGCCCACTACATCGTGTGTCTGTGGGTGGGGTGTGGGAGAAAGGAGCAGAGATCAGAGATGTAGAGATGTGGG  
 TGTAGAGTGTGCTCGGGGTACTCTTCAGATGTGCTCTCTAGTGTGATGAAGATCGAAGCATACACAGACTGT  
 CTAGTTCAGACACTGGTGTGTGATCAAGCGGGGAGCAGGAGACAGACAAGCTGTGCGACACTCCCGTCTCTTC  
 TCGAGCTCCCACTCACCTCTCCCTCGGCGACAGCCATCTTTTCAGCGCTCGAGCACATGGAAACCGCACTGAAGTCCCT  
 TCTCCACTTATGTGTCCAAAGGACATGAATCAACAGATACCAACTCTGTCTGCTGTGTAGAACCAAAGTATCTG  
 AGTAGCATTCAGGAGGGGACAGCTCCCTGACACACAGCTCAGCAGAGGGGGAGAGAGCTGGACACAGACCTC  
 CCAAACCTTCAGGTAGTCAAC CAGCAGAGCGCCCAACAGCAGCATCTCGAAGCTGTGCGCACTGATGAG  
 GCACTGTGGGGGCGAGAGCTTCAGCAGCGCCACTCAAGGCGCCCGAGAGGGGACATCTPAGACAGACCTTACACAG  
 CATTITGACATCAATGAGCATTTGCCGTGGATATGTGTCTTTTCTGCTGTGGTGTCTGTGGTGTATGTGGTGT  
 TCGAGTATCGGAAAGAGCTCGAGGACTGTAAAGAAAGGGGCGCGCGAGGATCCAGAGTGCCATTTGTGAAAGGACA  
 GGGCTGAAGAAATCATGACTACTCCAAACCGAGCCGGAAGATGGATCTACTGCAATGGCCATGGTATTCGAT  
 ATCTGAAGCTTTGTAGCAGCCAGAGTGGAGAGCGGAGAGAGATATCATAGTCTTTCTTGCAATGCCAGTGGAG  
 AGGGAGTGTGCTGTCTTCTCCAAATGGGTACAGCCGCCAGCAGGACCGCTAGCAGCTCTCTGACATCTGGAC  
 ATCCGGGGCGCGAGGCGACGCTCGCCGAGCATCTTGAGCCCTGTGCCGACACCGGAGAAACGATGTGTGGAG  
 AAGATTTCTGGGCTGTGAGAAACACCAACCACTTGGAAATGTAAACATAGCTCTCCGAGTGGAGGCCCGAGCGC  
 CTTAGCCGAGCCCATCCCGAGCCCAAGCAAGCAATGAGAAATCCGCTCTCCAGCAGGTGGAGCTCTCCCA  
 CAGGACAGAAACAGGCGCTCTCTCTGTGATGCTGCGAGCGCCCTCTCGCTGTGACTCTACCTACCGGCTCT  
 TCGCGCTGAGCAGGAAAGCGTTCTTTTATTCACAGAAAGAGAGACAGACTGTGCGGCGAGTGTGCTCTGGAC  
 CCTCTGAGCTTCGACGCTATCTTTGATGACAGTCTCCACTTCTTCAAATCTGAGGAGCTGCGGTGATGAAGAG  
 ATTCGCGAGCTGAGGACAACTTCAGACCGGCTATTCGAATTTATGAGTCAAGAGCCAGGAGGCCAGCAGACC  
 CTCTCGGACTCTGTTATAGCCATCTCTTCAGCTCTGCTGTGAACATAGGATATCGCATCTCGAAATTACTCA  
 ATTTAGTGTGCGAGGTGGTTTTAAATTTCTCTGTTTCTGATTTTGTGTTGGGGTGTGTGTGTGTTGTGT  
 GT  
 TCTCTCTCTTTTTTTTAAATAAATCTCTTGGGAAGTTGGTTTATAAGGCTTTGCCAGGTTGTAACTGTGTGA  
 ATACCCACCACTAAAGTTTTTAAAGTCCCAATTTTCTCCATTTTGGCTTCTTATGTATTTTCAAGATATTTCG  
 TGCACTTTAAATTTACTTAACTTACATAAATGCASTGTGACTTTTCCACACATGGATTTGTGAGGCTCTTAAC  
 TCTTTAAAGAGTATAGGCATCTGTGAATCTTAAATGCAAGCTCTTATGTCTTCTAACATCTCAACCTACTTTT  
 AAAAACCAATATATATATATATTTATTTATTTGTTGTCCTTATAAATTTCTAAAGATTAAGAAATTTAAGA  
 CCCCATGTAGTATCTGTAATGCAATCAACTTCAACTTTGAGTATTTTAAATATGTCTGTATGTTATATTCATGTAG  
 CTGAAATCTTGACCACATATCTGCTGATTTGATGTGTTTTCACCTGACACCGGTGATAGATCTGTGATTATGTAC  
 TCTCTTCTTATATATATGTCTGCGGCTGGGAGAAATGAATCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT  
 GACAACCTGGGCGCAAGAAGACTTGAACCTCACTTCACTTTTAGATTTAGAGTGTGTGAAACACATTTGCTGCACTT  
 GGAAGTGCAAAATCAAGTGCAGGTGGCGCCCTTCTCATAGAGAAATTTGCGAGCTTTGCTTTAAAGAGTGTCTGT  
 TTTTATATACATAATCAATGATGTCCAACTGTGCTCTCAAGCGCTTGGTCTGGTGGGATCTTCAACAAT  
 ACTTTTAAATTAAGTTCGCTGCAAGCTGTGAAGAACCTTGTCTGATATTTGCAACATTTGTCTCCCATTTCAAAGT  
 TACCTCTTAAAGTGTGAGTGTGACCTGCAAGTTCGAAGTGGATGTGCTGACCTCTTGTGTGGGTGGGTTTGTGG  
 GTAGTGTGTGAGGAGCCGATATCAGAAAAATGCCCTTCAGTGTACTAATTTATTAATAAACATTAGTGTGTTGTTA  
 AAAAAAATAA

## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594

><subunit 1 of 1, 655 aa, 1 stop

><MW: 71845, pI: 8.22, NX(S/T): 8

MGTSPPSSSTALASCRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTPTRHENGIEKCHDCSQCPWPPIEKLPCA  
ALTDRECTCPGPMFQSNATCAPHTVCFVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSPSSSTSPSPGTAIFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL  
KLLPSMEATGGEKSSSTPIKGPKRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNRKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYALQHWTIRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPLSPSPPIPSNAKLENSALLTVEPSQDKNGKGFVDESEPLL  
RCDSTSSGSSALSRRNGSFITKEKDDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEIIGVKSQEASQTLLDSVYSHLPDLL

### **Signal sequence:**

amino acids 1-41

### **Transmembrane domain:**

amino acids 350-370

09978192-101501

# FIGURE 27

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCGTTGGTGCCATCTACATTTTGGGA  
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC  
CATGGGGGAAAAATGATCCGCCTGCTGTTGGAAGCCCCCTTCTCATTCCGATCGCTTTTGGCC  
TTGATGATTTGAAAAAAGTCTCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG  
TCACTGCTGCCATTGAAGTTTTCCTCAATCATCGTCATTGGGATCATGTCATTGATATTAGC  
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC  
GAGTACCCTGTGTCCGGTGGGTGGTTCAGAATGCCGTGCTCCAGGTGTTCCAGACTGCTTC  
GTGGAAGACCATGTGCTCCGATGACTGGAAGGTCACACGCAAAATGTTGCCATTGGTCCCAAC  
TGGGTTTCCCAAGCTATGTGAGTTTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGAGTTT  
CGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGTCAGTGACAGCCT  
GTGGTTCATAGAAGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCTTGTCTCGCAG  
TGGCCTTGGCAGGCCAGCCTTCAGTTCCAGGGCTACACCTGTGCGGGGGCTCTGTCTACAC  
GCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
CCATCCAGGTGGGTCTAGTTTCCCTGTTGGACAATCCAGCCCCATCCCACTTGGTGGAGAAG  
ATTGTCTACACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCTTGCCCAACTCTGAAGAGA  
ACTTCCCGATGGAAAAGTGTGCTGGACGTGAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCCTGTCTGTAACACGCGGCGCTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
GGAGGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGGACAGCGGGGGCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAAG  
TTAGTGGGAGCGACAGCTTTGGCATCGGCTGCGCAGAGGTGAAACAAGCCTGGGGTGTACAC  
CCGTGTCACCTCCTTCTGGACTGGATCCAGAGCAGAGTGGAGAGACCTAAAAACCTGAA  
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCCTGAGGTGATGAAGACAGCCCGATCCTCCCT  
GGACTCCCGTGTAGGAACCTGCAACAGCAGCAGACACCTTGGAGCTCTGAGTTCCGGCACCA  
GTAGCAGGCCCGAAAAGAGGCCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTT  
GTTTTTTGTTTTTTTGAAGTGGAGTCTCGCTCTGTTGCCCAGGCTGGAGTGCAGTGGCGAAA  
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCTCAGCTTCCCA  
GTAGCTGGGACCAAGGTGCCGCCACCAACCCCACTAATTTTTGTAATTTTAGTAGAGAC  
AGGGTTTACCATTGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCTGCTT  
CAGCTCCCAAGTGTGGGATTACAGGCATGGGCCACACGCTAGCCTCAGCTCCTTTT  
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCTTCCCACTGGTCCAT  
CTGGTTTTCTCTCCAGGGTCTTGCAAAATCTCTGACGAGATAAGCAGTTATGTGACCTCAG  
TGCAAGGCCACCAACAGCCACTCAGAAAAGACGCACCCCAAGAGTGCAGAACTGCAGTC  
ACTGCACGTTTTTCTCTAGGGACCAGAACCAACCCACCTTCTACTTCCAAGACTTAT  
TTTTCATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAAGCCTATTTTCATGATTTCTT  
TGTAGCATTTGGTGTCTGGGATATTGTGCTTTGAGTCCAAATAATATGTTTCTTCCCT  
CATTGTCTGGCGTGTCTGCGTGGACTGCTGACGTGAATCAAAATCATCCACTGAAA

0978192.101501

## FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEFYRCVRVGGQNAVLQVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSI DHLLPDDKV TALHH  
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGMNMSLLSQWPWQASLQFQGYHLCGGSVIT  
PLWIITAAHCYVDLYLPKSWTIQGLVSLLDNPAPSHLVEKIVYHSKYKPKRLGNDIALMKL  
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR  
DVYGGIISPSMLCAGYLTGGVDS CQGD SGGPLVCQERRLWKLVGATSPFGIGCAEVNKP G VYT  
RVT SFLDWIHEQMERDLKT

### **Signal Peptide:**

amino acids 1-20

### **Transmembrane domain:**

amino acids 240-284

09070492.101501

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## FIGURE 30

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLALAGALLAPCEARGVSLWNQGRADEVVSASVRSGLWIPVKSFDSK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCYYHGHVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIBIANHVDKF  
YRPLNIRIVLVGVEVWMDMKCSVSQDPFTSLHEFLDWRKMKLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFGMNHDTLDRGCSCQMAVEK  
GGCIMNASTGYFFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFPGGQKCGNRFVEEGEE  
CDCGEPEECMNRCCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCFANVYLHDGHSCQDVGICYNGICQTHEQQCVTLWGPAGKAPAGICFERVNSAGDPYGN  
CGKVSKSFFAKCEMRDAKCGKIQCQGGASRPVIGTNAVSIETNIPLQQGGRILCRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRQCQNI SVFGVHECAMQCHGRGVNRRKNCHCEAHWAPP  
FCDKFGFGGSTDSGPIRQAEARQEAAESNRERGGQEPVGSQEHASTASLTLI

Signal peptide:

amino acids 1-28

09/01/92.10.15.01

### FIGURE 31

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANTTCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCAGTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCCAGTGTCCTTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCTGCCACCCATTCCATNTCCATCCAAG

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## FIGURE 32

CATCCTGCAACATGGTGAAACACGCGCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA  
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCTCGGCCCTCCC  
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGCCACAAACTTTTTAAGAAGTTAAT  
GAAACCATACTTTTACATTTTTAATGACAGGAAAAATGCTCACAATAATTGTTAACCCAAAA  
TTCCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA  
TACCAAAATATCAATAATACITATCTCTGGGTAAAAACCTCTTCTCATACCCCTGTGCTAACAA  
CTTTTAACAAAAAATTGTCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTATATGGG  
ACAGAAAAAAAACCAAGGAAAAAATCACGCCACTTGGGAAAAAAGATTGCAAAATCTGCCT  
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC  
TTGAATATAAGACCTACTTGTCTATCTCCCTGCACCAGCCAGGAGCCACCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAATGGGTAAAGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTGT  
CCTTTAACCAAGTATGCCGGAAGCTACTGCAGCCGAAACCAAAAGCCCTCCAACAGTGCCT  
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCAATTAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACATAAAACCGAATCCAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCAGTACTTTGGGAGGCCTAGGCCGCGGATCACCTG  
AGGTCAAGGAGTTTGAGACTAACCTGGCCAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATATTGACTGGGCGTGGTGGTGAAGTGCCTGTGATCCAGCTACTCAGGTGGCTGAAGCAGG  
ACATACACTTGAACCTAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT  
CACGCTGTAAATCCCGGCACCTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAAGAGATCA  
AGACCATCCTGGCTAATAACAGTGAAACCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCAGCTACTCGGAGGCTGAGGCAGGAGAAATAGCGTGAA  
CTCAGGAGGCGGAGCTTGCACTGAGCCGAGATTGCGCTACTCTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA



### FIGURE 33

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVVLAL

LHLYH

**Signal peptide:**

amino acids 15-27

09978192.101501

# FIGURE 34

GCCGCGGCGAGAGCGCGCCAGCCCCGCGCGC**ATG**CCGCGCGCCAGGACGCGCTCTCTCCGCTGCTGGCCCGGC  
 CGGCGGCCCTGACTCGGCTGCTGCTGCTGCTGCTGGGCACTGGCGCGCGCGGCGCTGGGGCGCCCGCGCCAGG  
 AGGCGGCGCGCGCGCGCGGAGCGGCCCGCCCGCGCAGACGGCGAGGACGGACAGGACCCGACAGCAAGACACC  
 TGTACACGCGCCACATGTTACGCA CGGGATCCAGAGCGCGCGCACTTCGTCTATGTTCTTCGCGCCCTGGTGTG  
 GACACTCGCACGCGCTGACGCGACTTGGAAATGACCTGGGAGACAATAACACAGCACTGGAAGATGCCAAAGTCT  
 ATGTGGCTAAAGTGAGCTGCACGCGCCACTCCGACGTGTGCTCCGCGCCAGGGGTCGCGAGGATACCCACCTTAA  
 AGCTTTTCAAGCCAGGCCCAAGAAGCTTGAAGTACCGAGGTCTCTGGGACTTCCAGACACTGGAAAACTGGATGC  
 TGCAGACACTGAACGAGGAGCGCAGTGACACGAGCGCGGAAGTGGAAACCGCCAGTCCCGCCGAGCTCAAGCAAG  
 GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCAAGGCGGACCACTTTATCAAGTTCTTCGCTC  
 CGTGTGTGGTCACTGCAAGGCGCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCTTGAACATTCGGAACCTG  
 TCAAGATTGGCAAGTTGATTGTGACAGCACTATGAACCTGTGCTCCGGAACCGAGGTCGTGGCTATCCCACTC  
 TTCTCTGGTCCGAGATGGGAAAAAGGTGGATCAGTACAAGGGAAGCGGGATTGGAGTCACTGAGGAGGATCG  
 TGGAGTCGCGAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGCTCACGCCCTCAGAGGCGCCGGTGTGGCAG  
 CTGAGCGCGAGGCTGA CAAGGGCACTGTGTTGGCACTCACTGAAAACTTTCGATGACACCATTTGCAGAGAGGAA  
 TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCAATTGTAAGACTCTGGCTCCTACTTTGGGAGGAACCTCTTA  
 AAAAGGAATTCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCATGCTGAACGGAATATCTCGAGCA  
 AGTATTCTGGTACGAGGCTACCCCACTGTTATTTGCTTTCCGAGGAGGGAAGAAAGTCACTGAGCAAGTGGAGGCA  
 GAGACCTTGACTCGTTACACCGCTTTGCTCTGAGCGCAAGCGAAAGACGAACCT**TAG**GAACACAGATTGGAGGTCA  
 CTCCTCTGCCAGCTCCCGCAACCTCGGTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTTCGCGTGGTGGCT  
 GTTCAGAAAGCAGAACTACTAGCGGTGAGGTATCTTTCTTGTGTGTGTTTTCAGAGCAACACACTCTACAG  
 ATTCCTTTATTAAGTTAAAGTTTCTCTAAGTAAATGTGTAACCTAGTCACTGTGTAAACATTTTCAGTGGCGATA  
 TATCCCTTTGAGCTTCTCTTGATGAAATTTACATGGTTTCTCTGAGACTAAATAGCTGTGAGGGAATAGAA  
 TTGCTGGAATTTTGTGGCTCTGAGTTGAGTGATTTTGGTGAAGAGGACATGCTCAAGCACTGTTTACCTGTC  
 CCAGAGTTCTGGAAGAGGTGGCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGTTCACAGTTCGACTCAATAC  
 TGTGTTGTCCTGAGCATGGAGCAGATTGAAATGCAAAACCCACACTCTGGAAGATACCTTCAGCGCGCTGTC  
 TGGAGCTTCTGTGTCGTGGAATACTTCTCTCAGTGTGAGAGGTTAGCGGTGATGAAGCGCGTACTTCTGACC  
 GTGCTGAGTAAGAGAAATGCTGATGCCATAACTTTATGTGTCGATCTTGTCAAATCAGTTACTGTTTCAGGGAT  
 CCTTCTGTTTCTCAGGGGTGAACAATGCTTTAGTTTCTCATGTAAACAGAGGCCACATGAACTGT  
 TGGATGCTCTCTTAGAAGGGTAGGCATGGAAAAATCCACGAGGCTCACTCTCAGTATCTCATTAACCTCATTTGA  
 AAGATTCCAGTGTATTTTGTCACCTGGGGTGACAGACAGAGCAGGCTTTCCAGGCTCGGGTATCCAGGGAGGC  
 TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCAGAGTTTCTGATTCTGTTTCTCAGTAGTCTCTTTAGAGG  
 CTGCTATACTTTGCTCTGCTTCAAGGAGGTGACCTTCTAATGTATGAAGATGGGATGCAATTGATCTCAAGAC  
 CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGACCGCTGTGGCAGCTGTGATGCGAGTGTCTCTTA  
 ACTCATGTGCTCTGTGATTAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAAGCTTAAGATA  
 GATAGGTGTTTGTCTTTTACCATGAGTACTTCCCAATAAACCACCTTTGATCCCAACACTCTTCAACCCACCT  
 CCCATACGCAAGGGGATGTGGATACTTGGCCAAAGTAACCTGGTGGTAGGAATCTTAGAAACAGAGCACTTATA  
 CTGTCTGTGAGGCAAGAGATAACAGCAGCACTCTGACACCGCTCTGCTCTAAAGGAAATCTTTATTAATCACG  
 TATGGTTACAGATAATCTTTTAAAAAAGCAACCTCTAGAGAGACCAACTGTCAAGAGCTTTGTGATCA  
 CACAACCTCAGCTTTGCATCACGAGTCTTGATTTCCAGAAATCAAAGTGTACAAATTTGTTTGTGTACACTAT  
 GATACCTTCTCAATAAATCTCTTTTAAAA

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## **FIGURE 35**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS  
KHLTYTADMFTHG IQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNMEDAKVYVAKVDCTAH  
SDVCSAQGVRGYP TLKLFKPGQEAVKYQGPRDFQTLNWNMLQTLNEEPVTPEPEVEPPSAPE  
LKQGLYELSSANFELHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT  
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA  
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA  
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

**Signal sequence:**

amino acids 1-32

09978192.101501

## FIGURE 36

CTTTTCTGAGGAACCAAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCATTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCTGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACCTCCCTCATCCT  
ACGTATTTGCTATTTTCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTCTCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAAAA

0978192.101504

## FIGURE 37

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQLGLDIDSRPTAEVCATHTISPGPKGDDGEKGDPEGEEG  
KHGKVGGRMGPKGIKGEGLGDMGDQGNIGKTGPICKKGDKEKGLLGIPGEKGKAGTVCDGGRY  
RKFGVQLDISIARLKTSMKFVKNVIAIGIRETEEFYIIVQEEKNYRESLTHCRIRGGMLAMP  
KDEAANTLIADYVAKSGFFRVFVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC  
VEMLSSGRWNDTECHLTMYFVCFIKKKK

**Signal peptide:**

amino acids 1-25

0978192.101501

# FIGURE 38

GGTTCTATCGATTGCAATTGCGCCACACTGGCCGGATCCTCTAGAGATCCCCTGCACCTCGAC  
CCACGCGTCCGCTGCTCTCCGCCCGTGTGGAGTGGTGGGGCCCTGGGTGGGAATGGGCGTGT  
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT  
CGGAAGGGAGGATCAGGGATGTTTGCAGAGCGCTGGAACGAGCGGTGCCGATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGGCCGAGTTGCGCTGGCTTCCGGCGGACTTGGCCCTTTCGGGTGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTTCGAGCTCGCGCCCTGGCCGCGGTGCGCGCCAGCCCGGAAGG  
TCCCGAGGGGGGCTGCAGCTTGGCTGGCGCTCGCGAACTGGCCAGCAGCGCCGCGCCGCG  
ACACCTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
AGGGCTGCACGCGCCTTCTTACGTGCGCTAGGCTGGGACTGGGGACCCGACGCGCGCGACAG  
CGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGAGCCGGAGATGCAGCGGCCG  
GAAGCGCGCGGAGTTTTCGCGAGGGGACGGTGCCCGCAGAGGTGGAGGAGCCGCCGCCCT  
CTGTCACTGGAGCAACTGTGGCGCTGCTCCTCCCGCTGGCCGAGAGTTTCTGTGGCTCTG  
GTTCCGGCTGGCCAAGGCGCGCTTGCACACTGCTTGTGCCACCGCCCTCGCGCGGGCC  
CCCTGCTGCATGCTCCCGAGCTGCGCGCGCGCGCGCTGGTGCTGCGGCCAGAGTTTCTG  
GAGTCCCTGGAGCCGACCTGCCCCGCTGAGAGCCATGGGGCTTCACTGTGGGCTGCAGG  
CCCAGGAACCCCACTGCTGCAATTAGCGATTTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACCTCTCTTCCCCCAGAGCATAACAGACACGTTGCCCTGTACATCTT  
ACCTCTGGCACCAAGGGCTTCCCCAAGGCTGCTCGGATCAGTCACTCTGAAGATCCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACTCGCCCTCCAC  
TCTACCACATGTCGGTTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCACTTCTGGGAAGATTGCCAGCAGCACAGGGGTGAC  
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACCTTGTCAACAGGACCCCGAGCAGGAGC  
AACGTGGCCATAAGGTCGGCTGGCAGTGGGCAGCGGGCTGCGCCAGATACCTGGGAGCGT  
TTTGTGCGGCGCTTTCGGGCCCTTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCTGGCTTTACAAGC  
ATATCTTCCCCTTCTCCTTGATTCGCTATGATGTCAACACAGGAGAGCCAATTCGGGACCCC  
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGTTAAGCCA  
GCAGTCCCCATTCTGGGCTATGCTGGCGGGCCAGAGCTGGCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
CACAAACCGAGGTGGCAGAGTCTTCGAGGCCCTAGATTTTCTTCAGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGCGATGAAGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTTGTCTGAGAACTTGCACCTTATGCCCG  
GCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCAAGAGACCTTCAACAGCAGCAGAA  
TTCGATGGCAAAATGAGGGCTTCGACCCAGCACCCTGTCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCTTCACTGCCCTTCAACACTGCCCCGTACAGCCCTCTGCGCAGGAAA  
CCTTCGAATCTGAAGAACTTCCACACTGAGGCACCTGAGAGGAACTCTGTGGGTTGGGG  
CCGTTGCAGGTGTACTGGGCTGTGAGGATCTTTTCTATACAGAACTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAGGAAAAAAG  
AAAAAAGGGCGCGCGGACTCTAGAGTGCACCTGCAGTAGGATAACAGGGTAATAAGC  
TTGGCCGCATGGCCCACTGTTTATTTCAG

09978192.101501

## **FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913  
><subunit 1 of 1, 730 aa, 1 stop  
><MW: 78644, pI: 7.65, NX(S/T): 2  
MGVCQRTAPWKEKSQLEAAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL  
LLKLHLWPQLRWLPADLAFVRLCCKRALRARALAAAADPEGPEGGCSLAWRLAELAAQ  
RAAHTFLIHGSRFRFSYSEAEERESNRAARAFRLALGWDWGPDGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGAAAPLSPGATVALLLPAGPEFLWLWFLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVPQYIGELCRYLVNQPP  
SKAERGHKVRILAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGA VGRASW  
LYKHIFPFSRLIRYDVTTGEPIRD PQGHCMATSPGEPGLLVAPVSQQSPFLGYAGGP ELAQGK  
LLKDVFRPGDVFFNTGDL LVCDDQGFLRFHDRTGDTFRWKGENVATTEVAEVEFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYPARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLS DPLYVLDQAVGAYLPLTTARYSALLAGNLR I

### **Type II transmembrane domain:**

amino acids 45-65

### **Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

### **CUB domain protein motif**

amino acids 254-261

### **putative AMP-binding domain signature**

amino acids 332-343

### **N-glycosylation sites**

amino acids 37-40 and 483-486

09978192.101501

## FIGURE 40

CCTGTGTTAAGCTGAGGTTTCCCTAGATCTCGTATATCCCAACACATACCTCCACGCACA  
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC  
GCTTGTCCATCTCCCTCCCGGGGAGCGCGCGCTCCACCTTTGCCGCACACTCCGGC  
GAGCCGAGCCCGCAGCGCTCCAGGATCTCGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC  
CCATGGTGGTTTAAAAACACTCTTTTCTCTCTCTCTCGTTTGTATGACCGTTTCCA  
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCAGCCAGCCCTTGTGGCTTGCCATCGT  
CCATCTGGCTTATAAAAGTTTGTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGCTCCCTCGG  
CTGGCAGAAGGGGTGACGCTGGGCAGCGGAGGAGCGCGCTGCCCTGCTGGCGGGCTTT  
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCAGAGCTGGATTGTATG  
TTGCACCATGCTCTTGGATCGGGGCTGTGATCTTCCCTCTTGGGGCTGCTGCTCTCC  
TCCCCCGCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCCGCCAGGCGTACGGTGCC  
AAGGGATTACGCTTGGCGGACATCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
TCCTCAGGAATATACATCTGACACCAAGAAAGTGAAGACAAGTTAAGCCCAAAAGCAAAC  
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTGTGCGCACCACTTTTGTGCCAGG  
CATAGAATAATTTGACGAATTTTCCGAGAGCTCTGGAGAATCGAGAAAAGTCACTAAATGA  
TATGTTTGTACGGACTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTGT  
TCACAGAGCTGAAAAGGTACTACACTGGGGTAAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTTGGGCTCGGCTCTCGGAACGGATGTTTCAGCTGATAAACCTCAGTATCACTTCACTGA  
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAAGTCAAGCCATTGGAGACGTGCCCC  
GGAAACTGAAGATTAGGTTACCCGCGCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG  
ACTGTGGGCAGAGAAGTTGCAAACCCGAGTTTCCAAGGTACGCCAACCCACAGGGTGTATCCG  
TGCCCTCATGAAGATGCTGTACTGCCCATAGTTCGGGGGCTTCCACTGTGAGGCCCTGCA  
ACAACTACTGCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT  
TGAGTCGCTATGGAACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCCAAACCTGCTCCAGCC  
CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACAGCTTTCAGGCCCTACAATCCTGA  
GGAAGACCAACAACTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCTTACACTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCACGTCACACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
GCCTGAGATCATGAATGATGGGCTCACCAACAGATCAACAATCCCGAGGTGGATGTGGACA  
TCACTCGGCTTGACATTTTATCAGACAGCAGATTATGGCTCTCGTGTGATGACCAACAAA  
CTAAAAACGCTCAATGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
CTCAGGAGTGGCAGTGGGTGATGGATGACGTGTGTCCACGGAGTTTGAAGTTTGTACCA  
CAGAGCCCCCGCAGTGGATCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCACAGCGTGGC  
CACTCCCTGCTCTCCTGGTCTCTCACTGCATTTGTCTTGGCAGTGCAGAGACTGTGCAGATA  
ATCTTGGGTTTTTGGTTCAGATGAACTGCATTTAGCTATCTGAATGGCCAACTCACTTTT  
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACCTTACCGTTTTCTATGAGAAGAGAG  
CAGTAATGCAATCTGCTCTCTTTTGTTTTCCAAAGAGTACCGGGTGCCAGAGCTGAAGTGG  
CTTCTCTTTCTCTCAGCTATCTGTGGGACCTTGTATTCTAGAGAGAAATCTTACTCAA  
ATTTTTCTGACCAGGAGATTTTCTTACCTTCATTGTCTTTTATGCTGCAGAAGTAAAGGAAT  
CTCAGTGTGAGGGTTTTTTTTTCTCAATTAATAAT

09978192.101501



## FIGURE 41

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADVKARSCGEVRQAYGAKGFSADIPYQEIAGEHLRICPO  
EYTCCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLENAEEKSLNDMF  
VRTYGMILYMQNSEVFQDLFTTELKRYTTGGNVNLEMLNDFWARLLERMFQLINPQYHFSEDY  
LECVSKYTDQLKPFQDVPVRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVKGC LANQADLDTEWNLFIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVS AKVFQCGQPKPAPALRSARSAPENFNTRFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDESVTAGTSNEEECWNGHSKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDVCPTEFEFVTTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

**Signal peptide:**

amino acids 1-23

09978192-101501

# FIGURE 42A

CGGACGCGTGGGCGGACGCGTGGGCAAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG  
CAGTTTGCAGCGCTCGCGCGGGTGGCCCACTACGCAAAAGACCAGCGGGCTCGCGCGGACCGGCCCGGGGCG  
TAGGGACCCGCGCTTTGGCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCAGGAAAACGGCTTCTTCTCACTTCGCGCTGCTGGTGAGTGTGCGGGGAGATTGGCAAAACGCTCAGG  
AAAGGACTGGGGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGCTCCACTACGGCAGTTTATCTG  
TCTGATCAGAGCCAGACGCGAGCGGTCCACTTCGCGAGTCTCTTCAGGTGTGGGGACCGCAGGACAGACGGCCGA  
TCCCGCCGCCCTCCGTACCCAGCACTCCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA  
AAAGTTCTGTCTCACTGTGATTCCTCAATTCTGCTTGGTTTTTTCTCCAGAGAACTTTGGGTGGAGATATTA  
ACTTTTTTCTTTTTTTTTTCTTGGTGAAGCTGCTCTAGGGAGGGGGAGGAGGAGAGAAAGTGAAATGTGTC  
TGGAGAAGAGCGAGCCCTCTTGTCTTCGGAGTCCATCCATTAAAGCCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTACCCTGTGTGGGTGCATG  
TGTGGCCCGCAGCGCGCGGGGCGGTGTTCTCCGCTGGAGTCTCACCTGGGACCTGAGTGAATGCTCCCCA  
GGGGCTGTGCGGGCATCGCCCTCGCTCTTCCACAGGCGCTGTCTGTCTTCCAGAAAGTGTCTAGCAATGGGGG  
CGCTGGCAGGATTCTGGATCTCTGCTCTCTCACTTATGTTACCTGTCTGGGCGCAGGCCCTTAGAAGAGGAGG  
AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCAGCACAACCTTCCACCTCCAGGCCCATCTCA  
TTTTCATCTAGCGGATGATCAGGATTTAGAGATGTGGGTACCAACGGATCTGAGATTAAACACCTACTCTTG  
ACAAGCTCGCTGCGGAAGGAGTTAACTGGAGAACTACTATGTCCAGCCTATTGACACCATCCAGGAGTCACT  
TTATTTAGGAAAGTATCAGATACACACCGGACTTCAACCTTCTATCATAGAACCTACCCACACCTACTGTTTAC  
CTCTGGACAATGCCACCTCACTCAGAACTGAAGAGGTTGGATATTCAACGCATATGGTGGGAAATGGCACT  
TGGGTTTAAACAGAAAAGATGCATGCCACAGAGAGGATTTGATACCTTTTTTGGTCTCCCTTTTGGGAAGTG  
GGGATTACTATACACTACAAATGTGACAGTCTTGGGATGTGTGGCTATGACTTGTATGAAAAACGACAAATGCTG  
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACTCAGAGAGTACAGCAAACTCTTACTTCCATA  
ACCCCAACAAAGCCTATATTTTTATATATCTGCCTATCAAGCTGTTTCACTCACCAGTCAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATATCAACATAAACAGGAGAGATATGCTGCCATGCTTCTCTGCTTAGATGAAGCAA  
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAAACAACAGCATATCATTTTACTCTTCAGATAATG  
GTGGCCAGCTTACGGCAGGAGGGAGTAACTGGCTCTCAGAGGTAGCAAGGAACATATGGGAAGGAGGATCC  
GGGCTGTAGGCTTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACCTGTGACACATCACTG  
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAAGTGAGGGTCTTCTGCTCACCCAGAGTAGATATTTGCAATAACATTGACCCCTATACCAAGGC  
AAAAATGGCTCTCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAAGCATCAGAGTGCAGCACTG  
GAAATGTCTTACAGGAAATCTCTGGCTACAGCAGTGGGTCCCGCTCAGTCTTCTCAGCAACCTGGGACCGAACCG  
GTGGCAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCAGAGCGACCCATATGA  
GAGGGTGAACCTATCTAAACAGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCAGAGTTCAACAAAC  
TGCAGTGCCGGTCAGGTATCCCCCAAGAGCCCAAGAGTAACCTTAGGCTCAATTGGAGGGGTCTGGGGACCATG  
GTATAAAGAGGAACCAAGAAAAAGAGCCCAAGCAAAATCAGGCTGAGAAAAAGCAAAAGAGGAAAGCAAAAAA  
GAAGAGAAACAGCAGAAAGCAGTCTCAGGTAAACAGCAAAATTTGGCTCGATAAATCTCGCTGGCTTAAAGGTCA  
GGCTGTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCGCCACACTGAAACCTGTCTGCTCAGTG  
CCAAGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGAGATGTTATTCTCTCGCTCCTTTAGAAAAAGTG  
GTGAGTCTCGAGTTCCACTGTGTGCTTCACTCAACTGACCAAAACACTGCTTTGAATATAGGAGGAGAACATA  
ACCTACCTCACTCAAGCATGCTAATTTGATGGAAGTTACAGGGTATGATTAATACTACCTTTGATAAATTAC

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# FIGURE 42B

AGTCAAAGATTGTGTCACTCAAAGGCCCTGAAGAATATATTTTCTGGTGAATTTTGTATGTCTGTCAATGA  
 CACTGGGTTTTTAAATTAATCTATTTTATATATATAAATATATGTTTCTTTTCTGTGAAAAGCTGTTTTCT  
 CACATGTGAACAGCTTGCACTCATTTTACCATGCGTGAGGAATGGCAAAATAAGAATGTTTGAGCACATGCC  
 ACAATGAATGTAACATTTTCTAAACACITTACTAGAAGAACATTTAGTATAAAAAACCTAATTTATTTTACA  
 GAAAAATATTTGTTGTTTTTATAAAAGTTATGCAAAATGACTTTTATTTTATTTTCTGCATACCATTAGAAGA  
 ATTTTATTTTCATTTCTTCAAATATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGGAATTCAGACTA  
 TAAAAAACATCATTCAGAAAACTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT  
 ATTACTTGGAATTCATGTTTGTGCGAGTTGAGACAACCTTTATGTTTCTATCATAAACTATTTATGTATCTT  
 AATTATTAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAAAT  
 GTATCATTTGGTCTAAAAAATAAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACAAACCACAGTAA  
 TATAATATGATTTTACAGATAGATGCTTCCCTTGGCTATGACATGGAGAAAGATTTTCCATAATAATAACTAA  
 TATTATATAGTGTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT  
 GGACACTGTGGGAGATACAGAGAAATGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAACCCC  
 ACATGCAACGCTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTGATCAATGAGCATA  
 GATTGGTGTGGATCCGTAGACCCGTGGTGTCTTTCTTGAAGTGCCCTCTCCTAATGCGAGAGCCCTGAAGCTTAC  
 AGTATACACTTGAAGGTACAGATAGCTAGAATTAATGATCTTTGAAGTTATAAATGTGATCTGAAAATGTGTGT  
 GGTGTATGACAGCATACCATTAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCAATTTATATCAC  
 AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAAGAACTCTATAAT  
 CTAGTACTGAAATTACTAAATGGGTAAGATGATTAAATGATTTTAATTTTAACATTTTATTTCTAGAATATAT  
 GGCTCCATTTTATTTTATAGTGAAGTTGTATTTCTTAAAGTTTGTGTTTGTGCGACAGTATCTTTTAAATGAG  
 TCTTAAAAATAAAGGCATATTGTTTATGTTTAAAAA  
 AA

09978392.101501

## **FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296  
><subunit 1 of 1, 515 aa, 1 stop  
><MW: 56885, pI: 6.49, NX(S/T): 5  
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYPHGSEIKTPTLDKLAAGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIIRPTQPNCLPLDNATLPQKLKEVGYSTHVMVGKWHLGFNREK  
MPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCYDLYENDNAANDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSPHQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA  
LKTYGFYNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGFVHSPLLKNKGTVCCK  
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQFSECSGNCLEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWYTLTGIIQES

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-37

#### **Sulfatases signature 1.**

amino acids 120-132

#### **Sulfatases signature 2.**

amino acids 168-177

#### **Tyrosine kinase phosphorylation site.**

amino acids 163-169

#### **N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

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# FIGURE 44

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGCGCGCGC  
 TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGCTCAGGAGGAGGAAGGAGGAC  
 CCGTGGCAGAAATGCTCTGCGCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCTGGGTGGCAG  
 GTGGTTTCGGGAACCGCGGCCAGTGAAGGCATCACGGGTGTTAGCATCGGCACGTGAGCCT  
 GGGGTCTGTCACTATGGAACATAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
 AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT  
 GCAGATGCTTTCAGGATACACCGGGAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG  
 AAACCCCGGCATGCCAACAGATGTGTGAATACACAGGAAGCTACAAGTGCTTTGCGCT  
 CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACTCTAGGACATGTGCCATGATAA  
 ACTGTGAGTACAGCTGTGAAGACACAGAAGAGGGCCACAGTGCCTGTGTCCATCTCCAGGA  
 CTCGGCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
 CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA  
 TTGGTTTCGAAGTCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
 ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGCTCCTTCAAGTG  
 TAAATGCAAGCAGGATATAAAGGCAATGGACTTCGGTGTTCTGCTATCCCTGAAAATTCCTG  
 TGAAGGAAGTCTCAGAGCACCTGGTACCATCAAAGACAAATCAAGAAGTTGCTTGTCTCAC  
 AAAAAACAGCATGAAAAAGAGGCAAAATTTAAAAATGTTACCCAGAACCCACCAGGACTCC  
 TACCCCTAAGGTGAACTTCGAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACT  
 CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGCTTGAGGATGAGAAAAGAG  
 AAGAGAAAGCCCTGAAGATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTCCCT  
 AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAGCGCTAACTTCCAA  
 ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT  
 GGAACAGGATAGAGAAGATGATTTTGAAGTGAATCCTGCTGATCGAGATAATGCTATTGGC  
 TTCTATATGGCAGTTCCGGCCTTGGCAGGTCACAAGAAAGACATTGGCCGATTGAACTTCT  
 CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTGTCTCTTTGATTACCGGCTGGCCGGAG  
 ACAAGTCCGGGAACTTCGAGTGTTTGTGAAAAACAGTAACATGCGCTGGCATGGGAGAAG  
 ACCAGAGTGAAGATGAAAGTGAAGACAGGGGAAATTCAGTTGTATCAAGGAACTGATGC  
 TACCAAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAAACCGGCGAAATCGCAGTGG  
 ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
 TTACTATCTTTTATATTGACTTTGTATGTGAGTCCCTGGTTTTTTGTATTGCATCATAG  
 GACCTCTGGCATTTTAGAATTACTAGCTGAAAAATTTGTAATGTACCAACAGAAATATTATTG  
 TAAGATGCCCTTTCTGTATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT  
 TCTCAGTCATTTCTGAATCTTTCNCATTATATTATAAAATNTGGAANGTCAGTTTATCTC  
 CCCTCCTCNGTATATCTGATTTGTATANGTANGTGTGNGCTTCTCTCAACATTCTTA  
 GAAAATAGAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGGA  
 AACTATGACATCAAAGATAGACTTTTGCTTAAGTGCTTACTGGGTCTTTCATAGCCAAAC  
 TTGTATATTTAATCTTTGTAATAATA

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## **FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNRNSKGVCE  
ATCEPGCKFGECVGPNNKCRCPGYTGKTCSDVNECGMKPRPCQHRVCVNTHGSKCFCLSGH  
MLMPDATCVNSRTCAMINCYSCEDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRVCNTFGSYYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMKKKAKIKNVTPEPTRTPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

### **Signal peptide:**

amino acids 1-21

### **EGF-like domain cysteine pattern signature.**

amino acids 80-91

### **Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

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## FIGURE 46

GGGAGCTGCTGCTGTGTGGCTGCTGGTGTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCCTGAGGGGCTGACGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC  
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCAGAGTGAATTTGGTGAAG  
AGCTGGCTTACCAGTTGTCTAACTAGGAGTTTCTCTTGTGCTGTGAGCCAGAAGAGTGCAT  
GAGCTGGAAGGGTGAAGAAGATGCCCTAGAGAATGGCAATTTAAAGAAAAAGATATACT  
TGTTTGGCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGAATGTCCAGCGTTCTCTGTGC  
ATGGATACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTC  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTAATGGCCCTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTTGTGGAGAATTCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC  
TTTAAGACAAAACATGCTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAAATAATAAAG  
ATTGCCATGAATCTTGCAAAA

09978192.101501

## FIGURE 47

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343  
><subunit 1 of 1, 289 aa, 1 stop  
><MW: 32268, pI: 9.21, NX(S/T): 0  
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGP  
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIFKTKHD

### **Important Features:**

#### **Signal Peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 136-157

#### **Tyrosine kinase phosphorylation site.**

106-113 and 107-114

#### **Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

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## FIGURE 48

GCGACGTGGGCACCGCCATCAGCTGTTTCGCGCGTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGTTGGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTTCGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCTCTGTGCC  
**TGATG**CTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTC  
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
GTGGCTCAGTTTCCGGAAGGTTCAAGAACCCAGGGCAAGGCTAAGAGGCACTGAGCCCTCA  
ACCCAAGCCAGGCTGACCTCATCTGCTTGTCTTGGTCTTCAAGCCGCTCAGCGTGCCCTGTG  
GACAGCGTGGCCCCCGCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCCAGTGGCCC  
TGGCAGGCCAGTGTGAGGAGCAAGGAGCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
CTGGTCTCTCACTGCTGCCCACTGCTTTGAAAGGCAGCAGCAACAGAACCTGAATTCCTGGT  
CAGTGGTCTCTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGTG  
GCTGCCCTGCAGTTGCCAGGGCCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCACCCACAGCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC  
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCACTGATGCTCCTGGGACC  
CTACGCAATCTGCGCCTCGGTCTCATCAGTCGCCCACTGTAACCTGTATCTACAACAGCT  
GCACCAGCGACACTGTCTCAACCCGGCCCCGGCTGGGATGCTATGTGGGGCCCCCAGCCTG  
GGGTGCAGGGCCCCCTGTCAAGGAGATTCCGGGGGCCCTGTGCTGTGCCCTCGAGCCTGACGGA  
CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTCTTGGCTGCAGGCTCGAGTTACAGGGGGCAGCTT  
TCCTGGCCAGAGCCAGAGACCCCGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCTCCAGGCAGGAGCACCTCCCATGGCCCTGGGAGGCCAGGCT  
GATGCACCAAGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGCGGTGCTAACTG  
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACAGA  
CCGGAGGAGTGGGGCTCAAGCAGCTCATCTGTCATGGAGCCTACACCCACCTGAGGGGG  
CTACGACATGGCCCTCCTGCTGCTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
TCTGCTGCCCTATCTGACCACCACTGCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG  
GCCGCCAGGAGCAGGCATCAGCTCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG  
GGCCTGCAGCCGGCTGCATGCAGCTCTTGGGGGTGATGGCAGCCCTATTCTGCCGGGATGG  
TGTGTACCACTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGACCACTGGTG  
CATGAGGTGAGGGGCACATGGTTCTTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
CCCCGCCAGGCCGGCGGTCTTACCGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG  
ACTGGCAGGTCTACTTCGCCGAGGAACAGAGCCGAGGCTGAGCCTGGAAGCTGCTTGCC  
AACATAAGCCAACCAACAGCTGCT**TGA**CAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
AGGCAGGCAAAATGGCATTACTGCCCTGTCTCTCCCACTGTCTGTCATGTGTGATTCCAGGCAC  
CAGGGCAGGCCCCAGAAGCCAGCAGCTGTGGGAAGGAACCTGCTGGGGCCACAGGTGCCCA  
CTCCCCACCTGCAGGACAGGGGTGTCTGTGGACACTCCCAACCCAACTCTGCTACCAAGC  
AGGCGTCTCAGCTTCTCTCTCTTTACTCTTTCAGATACAATCACGCCAGCCAGCTGTGTTT  
TGAAAATTTCTTTTGGGGGGCAGCAGTTTCTCTTTTAAACTTAAATAAATGTTAC  
AAAAATAAA

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## **FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVVQEPQGAKRHHGNTV  
PGEWFWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPHTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRLNRLRLISRPTNCIYNQLHQRHLSNPARGMLCGGPQPGVQGPCQGDSSGGPVLC  
LEPDGHVWQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPPEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLLAQPVTLGASLRPLCLPYPDHHLPDGERG  
WVLGRARPGAGISSLQTVPTVLLGPRACSRLLHAAPGGDGSPIILPGMVCTSAVGELPSCGELS  
GAPLVHEVRGTWFLAGLHSPGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEAP  
GSCLANISQPTSC

### **Important features:**

#### **Signal peptide:**

amino acids 1-15

#### **Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

#### **N-glycosylation sites.**

amino acids 37-40 and 564-567

#### **Kringle domains**

amino acids 79-96, 343-360 and 235-247

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## FIGURE 50

CGGGCCGCCCCCGGCCCCCATTCGGGCGGGGCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCGAGGGGAGCCTTCCACCACGGGGAG  
CCCAGCTGTGAGCCGCTCACAGGAAGATGCTGCGTCGGCGGGGAGCCCTGGCATGGGTGT  
GCATGTGGGTGAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCTGTGCTGCTCCTTCTCC  
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATACCAAACA  
GCTGGTGCACAGCTTGTCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGACGCGCTGCGTGTGGCG  
GACGAGGGCAGCTTCACTGTCTCGTGAGCATCCGGGATTTCCGGCAGCGCTGCCGTGAGCCT  
GCAAGTGGCCGCTCCCTACTCGAAGCCAGCATGACCTGGAGCCCAACAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCTGAGGCTGAGGTGTTT  
TGGCAGGATGGGACAGGTGTGCCCTGACTGGCAACGTGACCACTGCGAGATGGCCAAACGA  
GCAGGGCTTGTTTGATGTGCACAGCGTCTGCGGGTGGTGTGGGTGCGAATGGCACCTACA  
GCTGCTGGTGGCGCAACCCCGTGTGACGACAGGATGCGCACRGTCTGTACCATCACAGGG  
CAGCCTATGACATTTCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTGACCATGAGGACCAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCAACAGATGCATCTGTCTGACAGGTGGGCTCCTTCTCAAAGGATGCGATACAC  
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATCCCAAGTCATCTGCTGCCTTTT  
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCTGCTGCT  
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCCTC  
TTCTTCCAGTGTGCTGCTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTGAGA  
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCTTGTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTTCCAGCCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGGGCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCTTTT  
CCCTCCTTCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCACCCCAACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCTGGC  
TTGGCTCTGGCCAGTCTCTGGCCTCTGGTAGAGTGAGACTTCAGAGCTTCTGATGCCTTCCG  
GATGTCTCTCTCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTTGTAAACTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA  
AAAAAAAAAAAAA

## FIGURE 51

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALVQVPEDPVVALVGTDATLCCSFSPPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGDQGSAYANRTALFPDLLAQGNASLRLQVRVVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDQGQVPL  
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEENAGAEDQDGESEKSKTALQPLKHSKED  
DGQEIA

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Transmembrane domain:**

amino acids 251-270

#### **N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

#### **Homologous region to Immunoglobulins and MHC**

amino acids 217-234

09978192-101501

## FIGURE 52

TTCGTGACCCCTTGAGAAAAAGAGTTGGTGGTAAATGTGCCACGTCCTTCTAAGAAGGGGGAGTC  
CTGAACCTTGTCTGAAGCCCTTGTCCGTAAGCCTTGAACACTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTTCGCTGCTTTTGTAGGGACTTCTTCCCTTGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACTTCTTTGATTGGGGCTTTTGATCCCTGAACCA  
GAAGTGAAAAATTGAAGTTCTCCAGAAGCCATTTCATCTGCCATCGCAAGACCAAAGGAGGGGA  
TTTGTATGTTGGTGCACATATGAAGGCTACTTAGAAAAAGGACGGCTCCCTTATTTCACCTCCACTC  
ACAAACATAACAATGGTCAGCCCATTTGGTTTACCTGGGCATCCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAGGAATGTGTAGGAGAGAAGAGAAGCTCATCACTTCTCTGCTGC  
TCTGGGCTATGGAAAAAGAAGGAAAAAGGTAATAATCCCCAGAAAGTACACTGATATTTAATA  
TTGATCTCTCTGGAGATTGCAAAATGGACCAAGATCCCATGAATCATTTCCAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGCCTGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTGATAAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCCTTTTAAATATAGCACTCATCTTTCAAGAGAGGGCAGTCATCTTTAA  
AGAACATTTTATTTTTATACAATGTTCTTTCTGCTTTGTTTTTATTTTTATATATTTTTT  
CTGACTCCTATTTAAAGAACCCTTAGGTTTCTAAGTACCCATTTCTTCTGATAAGTTATT  
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACCTTTCACAG  
ATATGAAGCTTTGTTTTTACTTTCTCACTTATAAAATTTAAATGTTGCAACTGGGAATATACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCTATATTTCTGCTTCCCTCTATTTTTC  
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT  
GTTTATAATGAAATAGTTTATGTGTAACCTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTACTAAGGAGATGTGCAATGCTGAAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAG  
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTGAGACCGGCTGACCAACACGGAGAAA  
CCCTATCTCTACTTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAAATCACTTGAACCCGAGGCCAGGTTGCGGTAAAGCCGAG  
ATCACCTTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAAGAACCGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACTTAGGACTTAAGCTGATGAAGCTTTGGCTCCTAGTGAT  
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCTGTGTTCTTTAATGGGTAGTCTATAGTATATTATACATACAATAACA  
TTGTATCATAAGATAAAGTAGTAACAGTCTACATTTTCCATTTCTGTCTCATCAAAAAC  
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACTGGGTGAAACCTTGTCTCTA  
CTAAAAAATACAAAAATTAGCTCAGGCGTGGTGGTGACACCTGTAGTCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTGCTTGAACCCGGGAGGCGGAGGTTGTCAGTGAGCCAGATTTGTGCC  
ACTGCACTCGAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAGAAAGCAGAG  
CCTACAGCAGCTACTATTGAATAAATACCTATCTCTGGATT

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## **FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194  
><subunit 1 of 1, 211 aa, 1 stop  
><MW: 24172, pI: 5.99, NX(S/T): 1  
MRLFLWNAVLTLFVTSLIGALIPPEVKIEVLQKPFICHKRKTKGGDLMLVHYEGYLEKDGS  
L  
FHSTHKHNNQGPIWFTLGILEALKGWDQGLKGMCVGEKRKLIIPPALGYGKEGKGKIPPE  
ST  
LIFNIDLLEIRNGPRSHESFQEMDLNDDWKLKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDDKDGFISAREFTYKHDEL

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 176-179

#### **Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

#### **Endoplasmic reticulum targeting sequence.**

amino acids 208-211

#### **FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

#### **EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

#### **S-100/ICaBP type calcium binding domain**

amino acids 183-203

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## FIGURE 54

AATAAAGCTTCCTTAAATGTTGTATATGCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCCCACCGA  
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCTGGCTACCTCGCCCTGCCTTCAGCCT  
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGAGCATGGAGGTACAGTAC  
CTGCCACCCTCAACGTCTCAATGGCTCTGACGCCCCGCTGCCCTGCACCTTCAACTCCTGC  
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
TGAGGAGATGTTCTCCAGTTCCGCATGAAGATCATTAACTGAAGCTGGAGCGGTTTCAAG  
ACCGCTGGAGTTCCTCAGGGAACCCAGCAAGTACGATGTGTCCGTGATGCTGAGAAACGTG  
CAGCCCGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
CCATGGCAAGATCCATCTCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCTCCGTGCGGGGCTTCTGGCTGTGGTTCATCTTGGTGTGATGGTG  
GTCAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
GGAGGGCAAGACGGGACGGTGAAGGCCAACCCGGATGATGGCGCCAACTAGTGGGTGGCCGGCC  
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCG  
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGCCACCTGGGGCCTCCTGAACCCCG  
ACTTCGTATCTCCACCCTGCACCAAGAGTGACCCACTCTCTTCCATCCGAGAAACCTGCCA  
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCACCTGCCAGTCCCTGG  
GGGGAGGCAGGAGGCAATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
GGAGGGGCCGTGTACCTGCCCCAGTGCTTCCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG  
GGAGGGAGGGCTTCTCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCTGGCACGGCTG  
TGCTCCTCCCTGTCTCCAGCCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA  
AACTTGGAGGGGATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAGCCAGGG  
CTGCAGGCAAAAGCTGGACATGTGCCCTGGCCAGGAGGCCATGTTGGGCCCTCGTTCCATT  
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGGCATGTTTCCAGCGGGGACCCACCAACAGAGGCC  
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGTTGAATGCAGGTTGCTGCAG  
GCTCTGCCTTCTCCATGGGGTAACACCCCTCGCCTGGGCAGGGGCAGCCAAAGGCTGGGAAAT  
GAGGAGCCATGCACAGGCTGGGGCAGCTTTCTTTGGGGCTTCACTGAGAATCTCTCCAGTT  
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGAAGGGAAAGCCTGAGGCCG  
GCATAAGGGGAGGCCTTGGAACTGAGCTGCCAATGCCAGCCCTGTCCCATCTGCGGCCACG  
CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCAGCCCTGTAATCCAGCACTTTGGGAGGCCAAGCGGGTGGAATTACCTCCAT  
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG  
GTGGCGTGTGCTGTAATCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
GGAGCAGAGGTTGCAGTGAACCTGAGATAGTATAGTGCCATGCAATTCAAGCCTGGGTGAC  
ATAGAGAGACTCCATCTCAAAAAAA

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## **FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRVQPEDEGI  
YNCYIMNPPDRHRGHGKIHLQVLMEEPERDSTVAVIVGASVGGFLAVVILVLMVVVKVRRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 161-179

#### **Immunoglobulin-like fold:**

amino acids 83-127

#### **N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

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## FIGURE 56

GTTGTATATGTCCTGAAGTACATCOGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCTCCAG  
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCAGCAAGTACGATGTGTGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAAC TGCTACATCATGAACCCCC

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## FIGURE 57

TCACGGGGCTCATCTCTTTTCTCTTTGGTGCCCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCCTCAACGTCTCTCAATGGCTTTGACGCGCCCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACTGCTACATCATGAACCCCCC

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# FIGURE 58

TGCGGCGACCGTCGTAACCAATGGGCCTCCACCTCCGCCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT  
 TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGAGCGTCACCCCCCAGTGTGCTGGTCC  
 CTGGTGATTTGGGTAAACCAACTGGGAAGCCAAAGCTGGACAAGCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA  
 CCGAAAGCTACTTCAACAATCGGCTGAACCTGGAACTGCTGCTGCTCATCATTGACTGCTGGATTGACAAATA  
 TCAGGCTGGTTTACAACAAACATCCAGGGCCACCCAGTTTCTGATGGTGGAGTGACGTGTCCTGGCTTTG  
 GGAAGACCTTCTCACTGGAGTTCTCGGACCCAGCAAAAGCAGCGTGGGTTCTATTTCACACCAATGGTGGAGA  
 GCCTTTGTGGGCTGGGGCTACACACGGGTGAGGATGTCGAGGGGCTCCCTATGACTGGGCCGAGGCCCAAAATG  
 AAAACGGGGCCTACTTCTGGCCCTCCGCGAGATGATCGAGGAGATGTACAGCTGTATGGGGGCCCTCGTGGTGC  
 TGGTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGACGCGGACCGCAGGCTGGAAAGGACAAGT  
 ATATCCGGGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAAGCCCTGCGCGTCTGGCTTCAGAG  
 ACAACAACCGGATCCAGTCATCGGGCCCTGAAGATCCGGGAGCAGCAGCGGTGAGTGTCTCCACAGCTGGC  
 TGCTGCCCTACAACCTACACATGGTCACTGAGAAGGTGTTCTGTGACAGACCCACAATCAACTACACACTGCGGG  
 ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCGAGGACACAGAAGGGCTGTGTGG  
 AAGCCAGATGCCACCTGGCGTGCAGCTGCCTCTATGGTACTGGCGTCCCCACACAGACTCCTTCTACT  
 ATGAGAGCTTCCCTGACCGTGACCCCTAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACCTTGAAGAGTGCCC  
 TGCAGTGCCAGGCTGGCAGAGCCCGCAGGAGCACCAAGTGTGCTGACGAGGCTGCCAGGCAGCGAGCACATCG  
 AGATGCTGGGCCAACGCCACCAACCTGGGCTTACTGAAACGTGTGCTCCTTGGGCCCTGACTCCTGTGCCACAGGA  
 CTCCTGTGGCTCGGCCGTGAACCTGCTGTTGGCTCTGGGGCTGTCATGGGCCACGCGTTTGCAGAAAGTTGTGA  
 CTCACCATTCAGGGCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAAGTGTGTTTGTATCCTTCTCT  
 GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCGAAGATGCTGCTGATGGTGA  
 ACTGCTGTGACCTTAGACTGGCTCCACAGGTGGACTGGCTGGGCCCTGGTCCAGTGTGCTGCTGGGGCCATG  
 TGTCCCCCTATTCTGTGGGCTTTTACATACTTGCCTACTGGGCTCTGGCCCCCGCAGCCCTTCTATGAGGGAGTGT  
 ACTGGGCTGTGGTCTGTATCCAGAGGTCCAGGGATCGCTCTGGCTCTGCTGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
 GCCACAGATAGGCTCGCACTGGTCTAGGGTAGCTAGAGCTGCTGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
 TGACTGGCTTCTGGGCGAGCCCTAGTACTCTGACGGCAGGGGCGAGTTTGTGCGTCTCTGCTGGTTCACAGGC  
 CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACAGGAGCATTCAGCTCTGGATTGGGCAGCAGATGTG  
 CCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTCAAGCTGC  
 CTCCTTCAACCTGGGACTGTGTTCCAAAGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTTATGGA  
 GAAAGGGAATCCAAAGGAAGCAGCCAAAGGCTGCTGCAGCTTCCCTGAGCTGCACCTCTTGTAAACCCACATCA  
 CACTGCCACCTCGCTTAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGCTGAGGATGGGGCTCCTATCAC  
 CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCAGAAACTTGAATGGGACCTGAGAGAGCCAGGGGTCCCC  
 TGAGGGCCCCCTTAGGGGCTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGCTGGAGAGT  
 CAGGGCTGCCTTCACTGCGAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCGAGAAAAGGGTACAGCCCTCTAGGT  
 GGGGTTCCCAAGAGCCCTCCAGGCTGAGCTGCTCTCCACAGGGTTTCTGTGAGCTGGATTTCCTCTGT  
 TTGCATACCTGCTGGCATCTGTCTCCCTTGTCTCTGAGTGGCCCCACATGGGCTCTGAGCAGGCTGTATCTGT  
 GATTCTGGCAATAAAGTACTCTGGATGCTGTAAAAAAGGAAAAAAAAAAAAAAAAA

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## **FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189  
><subunit 1 of 1, 412 aa, 1 stop  
><MW: 46658, pI: 6.65, NX(S/T): 4  
MGLHLRPYRVGLLPDGLLFLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSSKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDRVPGFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNMRI  
PVIGPLKIREQQRSASVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWL  
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

### **Important features:**

#### **Signal peptide:**

amino acids 1-28

#### **Potential lipid substrate binding site:**

amino acids 147-164

#### **N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

#### **Lipases, serine proteins**

amino acids 189-201

#### **Beta-transducin family Trp-Asp repeat**

amino acids 353-365

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## FIGURE 60

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGGACGGCGACATGGAGAGCGGG  
GCCTACGGCGCGGCCAAGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCGCTGTGCTTGGTCTTCGCCTTGATCGTGTCTCTGCATCTATGGTG  
AGGGCTACAGCAATGCCACGAGTCTAAGCAGATGTACTGCGTGTTC AACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGGTTGGTTTCTGCTTCCTCACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCGGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCCTTCAACCAGAA  
CGCGGAGACCACCGAGGGCTACCAGCGCCCCCTGTGTACTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCTCTGCCCCTGGACTTTCCCATCAGCCTCCTGGAATGCCA  
GCCCCCTCTTTTACCTGTTCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCCTGTGCCGAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAAATGA  
CCTCAGCCCCGCTGCAGTGGCTAGAAGCCAGCAGGTGCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGCGCCGGGTGAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGCCATCACACCTGCCCTGTGCAGCGAGCCGGACCAGGCTCTGTGTCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGCTGGTGTCTATGGCACTTCTCCTTG  
CTCCACCCCTGGCAGCAGGGAAGGGCTTTGCCCTGACAACACCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCAGACTCTGTC  
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

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## FIGURE 61

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAGAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYEGEGYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLIGDLLFSALWTFWLVGVGFC  
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

### **Important features:**

#### **Type II Transmembrane domain:**

amino acids 1-45

#### **Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

#### **N-glycosylation site.**

amino acids 97-100

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# FIGURE 62

GAGCCACCTTACCTTGCTCCGAGGCCAGGCCCTCAGGGGCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG  
 CCCGTGGCCGAGGCCCCCGAGGTGGCTGGCGGGCAGGGGGACGAGGGTGATGGCGAGGAAGCGGAGCCAGAGGGG  
 ATGTTCAAGGCTGTGAGGACTCCAAGAGAAAAGCCCGGGGCTACCTCGCTCGTGGTCCCTGTTTGTGCTGCTG  
 GCCCTGCTCGTGTGGCTTCCGGGGGGGTGCTACTCTGGTATTTCTTCAAGGTAACAAGGCCGAGGGTGTATGGTCAGC  
 CAGGGTACTCAGGCAAGCTCTGGGTGACTCAATCGCCACTTCTCCAGGATCTTACCCGCGGGAGTCTAGTGCC  
 TTCCGAGTGAACCGCCAAAGCCCAAGAGATGCTCAAGGAGCTCATCACCAGCACCCGCTGGGAATCTTACTAC  
 AACTCCAGCTCCGTCTATTCTTTGGGGAGGGACCCCTCAGCTGTTCTTCTGGGTCTATTCTCCAAATCCCGAG  
 CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGAGGCATGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC  
 TCGGCTGCGCTGCCCTACAGGGCCAGGTACGAAGTGGACCCCGAGGGCTTAGTGATCTCTGGAAGCCAGGTGTGAAA  
 GACATAGCTGACATTGAATTCCACGCTGGGTGTGTACCGCTACAGTACGTTGGGCCAGGGCCAGGTCCTCCGGCTG  
 AAGGGGCTCCGACTCCGCTCAGCTGCGCTGTGGCACTGCGAGGCCCAAGGAACCTCATGCTCAAACTCCGG  
 CTGGAGTGGACGCTGGCAGAGTGC CGGGACCGACTGGCCATGTATGACGTGGCGGGCCCTGGAGAAAGGGCTC  
 ATCACCTCGGTGACGCGTGCAGCCGCGAGGACCCGTGGTGGAGGTTCTGGCGTGGGGGCCATCATGGCGGTC  
 GTCTGGAAGAAGGGCTGCACAGCTACTACGACCCCTTCGTGCTCTCCGTGCAGCCGGTGGTCTTCAAGGCTGT  
 GAAGTGAACCTGACGCTGGACAAAGGCTCGACTCCCGAGGGCTCTCAGCACCCGTACTTCCCGAGCTACTAC  
 TCGCCCCAACCCACTGCTCTTGGCACTCAGGTCGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGTAGCC  
 TATGCACTGAGGAGGCAGAAATATGATTTGCCGTGACACCGAGGCCAGTGGACGATCAGAAACAGGAGGCTGTGT  
 GGCCTGGCGATCTGCGAGCTACGCGAGAGGATCCCGGTGGGCCAGGGCCGGATCACCATCAACTTCCACC  
 TCCAGATCTCCCTCACCGGGCCCGGTGTGGGGTGCACTATGGCTTGTACAAACAGTCGGACCCCTCGCCTGGA  
 GAGTCTCTGTTCTGTGAATGGAATCTGTGTCTGCTGTGATGGGGTCAAGGAGTGCAGCCACCGCTCTGGAT  
 GAGAGAAACTGTTTGCAGAGCCACATTCAGTGCAGAAAGGACAGCACTGCATCTCACTGCCCAAGTCTGT  
 GATGGCGAGCTGATTTGCTCAACGCGAGCGATGAAGAGCAGTCCAGGAAGGGGTGCCATGTGGGACATTTCCAC  
 TTCCAGTGTGAGAACCGAGTCTGCTGAAGAAGCCCAACCCGAGTGTGATGCCACAGGACCTGTGCAGCGAGC  
 TCGGATGAGGAGCACTGTGACTGTGGCTTCAAGGGCCCTCCAGCCGATTTGTGGTGGAGCTGTGTCTCTCGAG  
 GGTGAGTGGCCATGCGAGCCAGCTTCCAGGTTCGGGGTCCGACATCTGTGGGGGGCCCTCATCGCTGACCGC  
 TGGGTGATAACAGCTGCCACTGCTTCCAGGAGGACAGCATGGCCCTCCAGGTGCTGTGAGACCGTGTCTCTGGGC  
 AAGGTGTGGCAGAACTTCGCGCTGGCTGGAGAGGTGTCTTCAAGGTGAGCGCTGCTCTCTGCAACCCTGAC  
 CAGAGGACAGCCATGACTACAGCTGGCGCTGCTGCGAGTGGCGCTGCTGCGAGTCCGACCCGCTGCGCGCC  
 CCGCTGCTGCTGCCCCGCGCTGCCACTTCTTCGAGCCCGGCTGCACTGCTGGATTACCGGCTGGGGCGCCTTG  
 CGCGAGGGCGGGCCCATCAGCAACGCTCTGAGAAAGTGGATGTGCAAGTGTATCCACAGGACCTGTGCAGCGAG  
 GCCATGCTGCTACAGGTGACGCCACGATGCTGTGTGCGGCTACCGCAAGGGCAAGAGGATGCCCTGTCAAGGT  
 GACTCAGGTGGTCCCTGTGTGCAAGGCACTCAGTGGCGCTGTGTTCTGGCGGGCTGGTCACTGGGGCTG  
 GGCTGTGGCGGGCTTAATCTTCCGCGCTTACACCCGATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG  
 ACCTGAGGAATGCCCCCTGCAAAAGCAGGGCCACCTCTGGACTCAGAGAGCCAGGGCACTGCGCAAGCAGG  
 GGGCAAGTATTCTGGCGGGGGTGGGGGAGAGAGGAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC  
 CTGATGTGCTGCTCCAGTGATGGCAGGAGGATGGAGAAGTCCAGCAGCTGGGGGTCAAGACGTCCTCTGAGGACC  
 CAGGCCACACCCAGCCCTTCTGCTCCCAATTCTCTCTCTCGTCCCCTCTCTCACTGCTGCTCAATGCAAG  
 GCACTGGCTCAGCAGCAAGAAATGCTGTTCTACATCCGAGGAGTGTCTGAGTGGCGCCCACTCTGTACAGAGG  
 CTGTTTGGGCAAGCTTGCCTCCAGAGAGCAGATTCCAGCTTGGGAAGCCCTGGTCTAACTTGGGATCTGGGAAT  
 GGAAGGTGCTCCATCGAGGGGGACCTCAGAGCCCTGGAGACTGCCAGGTGGGGCTGCTGCCATGTAAAGCCAA  
 AAGGTGGGGAAGTCTGACTCAGAGGTCCTTGGCCCAACCCCTGCTGCCACTGGGGCTCAGAGCCAGACCCCT  
 CACTGGGAGTGAGCTGAGCTGCCCTTTGGAATAAAGCTGCTGATCAAAAAAAAAAAAAAAAAAAAA

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## FIGURE 63

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 88846, pI: 6.41, NX(S/T): 7  
MPVAEAPQVAGGQGDGGDGEEAEPEGMPKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVMSQVYSGSLRLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT  
YYNSSSVYSFGEGLPTCFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGVRLRKGPDLHLASSCLWHLQGPKDMLM  
KLRLLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSSTPYFPSYSPQTHCSWHLTVPSLDYGLAL  
WFDAYALRRQKYDLPCTQGQWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRAFQCKEDSTCIS  
LPKVCDDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDDEHCD  
CGLQGPPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIA DRWVITA AHCFQEDSMASVTVL  
WTVFLGKVQNSRWPEGVSPFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG  
KKDACQGDGSGGPLVCKALSGRWFLAGLVSWGLGCRPNYFGVYTRITGVISWIIQQVVV

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 46-67

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 604-609

#### **N-glycosylation sites.**

amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512

#### **Krinkle domains.**

amino acids 746-758 and 592-609

#### **Homologous region to Kallikrein Light Chain:**

amino acids 568-779

#### **Homologous region to Low-density lipoprotein receptor:**

amino acids 451-567

0978169.101501



## FIGURE 64

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCGGTGTGCGGGTGCACTATGGCTTGTAACAACAGTCGGACCCCTGCC  
CTGGAGAGTTCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGAGAGCCACATTCCAGTGCAAAGAGGA  
CAGCACATGCATCTCACTGCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCTTCAGTGTGAGGACCGG  
AGCTGCGTGAGAAAGCCCAACCCGAGTGTGATGGGCGGCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTTCGGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCCTGTTCTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCTGCTCCTGCACCCGTACCAAGAGGAGACAGCCAT  
GACTACGACGTGGCGCTGTGTCAGCTCGACCACCCGGTGGTGCCTCGGCCGCGCTGCGCCC  
CGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCCGGCCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCACAGGACCTGTGCAGCGAGGCCTATCGTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTGAGGGTGAAGTCAAGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCTTGCGGGGCTGGTCAAGTGGGCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCTGCAAAGCAGGGCCACCTCCTGGACTCAGAGAGCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT

## FIGURE 65

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG  
CTCCGTGCGCGCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCAGCCCTTGCCG  
AGAGAAGGGTCTTACCGGCCGGGATGCTGGAAACACCAAGAGGTGGTTTTTGTTTTTTAA  
ACTTCTGTTTTCTTGGGAGGGGTGTGGCGGGCAGGATGAGCAACTCCGTTCCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTGCGGCCACAG  
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTACGGAT  
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCAACAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGCCGACATCCACAAGAGGCTCTCTCCGACGATGCAGATTTTG  
TGGATGTCCTCCACACCTACACGCTTCCTTCGGCTTGAGCATTTGTTATTAGATGCCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTTGCTTCCAGTGCACT  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGTCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAATCGTTGCAATCAGATTACACTGTGTCATGTCTAGGAAAGGGAATCTTT  
ACAAAAATAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAA

0978192-101501

## FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646  
><subunit 1 of 1, 354 aa, 1 stop  
><MW: 39362, pI: 8.35, NX(S/T): 2  
MSNSVPLLCFWSLCYCFAAGSPVFPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRTSKDPEHE  
GCYLSVGHSQPLEDCSFMNTAKTFFIIHGWTMSGIFENWLHLKLVSAHHTREKDANVVVDWL  
PLAHQLYTDVNNTRVVGHSAIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV  
GRITGLDPAGPMFEGADIIKRLSPDDADFVDVLHTYTRSFGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLFVDSLVDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Lipases, serine active site.**

amino acids 163-172

#### **N-glycosylation sites.**

amino acids 80-83 and 136-139

0976192.101501

# FIGURE 67

CGGACGCGTGGGCGGACGCGTGGGCTGGGCAAGGGCCGGGGCGCCGGGCGAGCCACTCTTCCCTCCCCCGC  
 TTCCTCTGTCCGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGCGCGCTTGGGGCTGACAGT  
 CGGCAAAAGTTTGGCCCGAAGAGGAAGTGGTCTCAAACCCCGCAGGTGGCGACAGAGCCAGAGCGGGCGCTCG  
 CTGCTCTGGGGCGGGCTGTAGGCGAGGGCGCGGCCCAAGTGGCGAGACCGGGGCTCTCAGGAGCCGGCCCGGGAG  
 AGAAGAGTGGGGCGGGACGAGGAGAAACAACCTCAAAGTTGGCGAAAGGCACCGCCCTACTCCCGGGCTGCGG  
 CGCGCTCCCGGCCCCAGCCTGGCATCCAGAGTACGGGTGAGCCCGGGCCATGGAGAGCCCCCTGGGAGGGCGG  
 CACCAGGAGCTCTGGGGCGCGGGGCTCGCGCGGACCCCATCGGGTGAACCAAGAGCTCCGGGACCTTCCG  
 GCACCTCTGGACAGCGCAGGATGCTGTGGGCCACCTCTCTCTCTCTCTCTGGAGGGCTCTGGCCCATCCAG  
 ACCGGATTATTTTCCAATCATGCTTGTGAGGACCCCCAGCAGTGTCTTAGAAGTGCAGGGCACCTTACAGA  
 GGGCCCTGGTTCGGGGACAGCGCACCTCCCTGCAACTGCACCTGGCTCACTCTGGGACGAGGAACAGACTCT  
 TCACATCAGGTTTCAGAAAGCTACACTGGCTGGCTGGCTCAGAGCGCTTAAACCTACGCTCCCTCTCCAGCCAC  
 TGATCTCCCTGTGTGAGGACCTCCAGCGCTCTGCGAGCTGCCGGGGGCAACGTCACCATCACTTACAGCTATG  
 CTGGGGCCAGAGCACCCATGGGCGAGGGCTTCTGCTCTCTACAGCCAGAGATTGGCTGATGTGCTCGAGGAAG  
 AGTTTCAGTGCTGAACACACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTGTGATGCTGTGGCGATGGCT  
 CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCTGACCCCAAGACCCGTCCTCCCTCCCTGCTTGAATG  
 TCACCTTGGAGGACTTCTATGGGGTCTTCTCTCTCTCTGGATATACACACTAGCCTCAGTCTCCACACCCCACT  
 CCTGCCATTGGCTGTGGACCCCATGATGGCCGGCGGCTGGCGGTGCGCTTACAGCCCTGGAGCTTGGGCTTTG  
 GAGATGCAGTGATGTGTATGACGGCCCTGGGCGCCCTGAGAGCTCCCGACTACTCGGTAGTCTCACCCACTTCA  
 GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTGTCTCTACACACAGTTGCTTGGAGCA  
 ATGGTCTGGGCTTCAATGCCACTTACCATGTGGGGGCTATTGCTTGCCTGGGACAGACCTGTGGCTTAGGCT  
 CTGGCTGGGAGCTTCAAGAGGCTAGGTGAGCGCTGCTACAGTGGGCACTGACGCGCTCATGCGGCTCATGGGCT  
 GTGCTGCCGACAGATGAGGAGGAGCTGCCAGGCTGCCACCTGGACACTTCCCTGTGGGCTGTCTGGCACT  
 CTGGTCCACAGCTGCTCACTGCTGCTGACCGGCTCAACTACAGACTTCTCTGCTGATGGAGCAGATGAGA  
 GACGCTGTCCGACTTGCACCTGGCAATTTCCGATGCCGGGACGAGAAGTGGCTGTATGAGACGTGGGTGTACG  
 ATGGGACGACAGCTGTGCGGACGGCAGTGATGAGTGGGACTGCTCTATGTCTTCCGCCCGCAGGCTTGCACAG  
 CTGGCTCATGGCAGTACAGCTCTTTGCCCCCTCTCCCGGATGGAGCTGGAGCTTGTGACAGCAGGCAACCC  
 TTTCCCTACGGGCGACTTATGGCCAGGGTGCCATCCCACTCTAGAGAAGCTTTCTACAGAGAATCCTATGATA  
 ACTCAGTGCTGGGCAACCTGCGTCTCTGCTACAGATCTTAGCGCAGGATAGACTCCAGGAGGTGGCCAGGCTG  
 CCGCGCTGTGTCAGCGGGGCGCTTGTATGCGACCGCTGGTAGCGCGCTCCGCGCTGGGCTTGTCTCCCTCGAA  
 CCAACACCCCGGCTCGGGCTCTGAGGCCAGATCCCAAGTTCACACTTCTGTGCTGCCCTTGGGCGCTTAGATG  
 GTGGCACAGTTCAGCCCGTGGGGCGGGGCASTGGTGGGCAAGATGGGGAGCAGGACCCCACTGCCCATCA  
 AGGCTCCCTCCCATCTGCTAGCACGCTCTCAGGCCCACTACTGCTCCCTGAAGCCCGAGGCCACTGCCCTCAC  
 TGCCCTTAGAGCCATCACTATTGTCTGGAGTGTGACGGCCCTGCGAGGCGCGCTGTGTGCCAGCTTGGGCGCC  
 CAGGACCAACCCGGAGCCCGCTGGACCCCAACAGCAGTCTCTGGCCCTGGAAGATGAGGACGATGTCTACTGG  
 TGCCACTGGCTGAGCGGGGCTGTGGGTAGCTGAGGACAGGATGAGCCACTCTTACTGAAGGGGAGTGGGG  
 CTCTACTGAGGCTCTCCCTCGGGGCTCTACTCATAGTGGACAACTTTTAGAGGATGGGTGAGCTCCCTCC  
 ACCACTTCTTCCCTGTCCCTGGATTTCAGGGACTTGGTGGGCTCCCGTGAAGCTATGTAGTGTCTATAAAGT  
 TAAGTGTCCCTCAGGCGAGGAGGGCTCAGAGAGTCTCTCTGTACGTGGCCATGGCCAGACACCCAGTCCCT  
 TCACACCACTGTCTCCACGCCACCACTTTGGGTGGCTGTTTTTAAAGATGAAGTTCTTAGAGGATCATAG  
 GGTCTGGACACTCATCTTGTCCAAACCTTACCCAAAGTGGCTTAAAGCACCGGAATGCCAATTAACCTAGAGA  
 CCTCTCCGCCCCCAAGGGGAGATTGGGCAGAACCTGAGGTTTTTGCCATCCCAACTCTCTACAGGGCTCG  
 CTCACAAAAGAGTGCACAAATGCTCTATTCATAGCTACGGCATGTCTCAGTAAGTTGAGGTCAAAAATAAA  
 GGAATCATACATCTC

09978192.101501

## **FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLGGALAHDPRIIFPNHACEDPPAVLLEVQGTLQRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPLQLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCGDGVDACGDGSDEAGCSSDPFPGLTPRP  
VPSLPCNVNTLEDFYGVFSSPGYTHLASVSHQPQSCHWLLDPHNGRRLLAVRFTALDLGFGDAVH  
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLSGSLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRCRDEKCVYETWVCDGQPCADGSDEWDGS  
YVLPKRVITAAVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQAPP  
SYGQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQLLRQDMTPGGGPGARRRQGRMLMRLVR  
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPAREGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPITTVPEAPGPLPSLPLEPSLLSGVVQALRGRLLPSLGPPGPTRSPPGPHTAV  
LALEDEDDVLLVPLAEPGVWVAEAEDEPLLT

**Important features:**

**Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

00378192.101504

## **FIGURE 69**

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTTGCTATCGCTTCG  
CAGAACCCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGAATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTATTTTTTCATA  
CTTTTATATGTACTCAGACTTGATCGATTAATGAAGTGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTATCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAAAGAAGTTTGTAATTTTTATATTACTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAAAAAAAAAAAAAAAAA

0978192.101501

## **FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645  
><subunit 1 of 1, 152 aa, 1 stop  
><MW: 17170, pI: 9.62, NX(S/T): 1  
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTLTVGGGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

### **Important features:**

#### **Potential type II transmembrane domain:**

amino acids 26-42

#### **Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

#### **Leucine zipper pattern**

amino acids 78-99 and 85-106

#### **N-myristoylation site.**

amino acids 110-115

#### **Ribonucleotide reductase large subunit protein**

amino acids 116-127

09970397-101301

## FIGURE 71

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAACATCGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAAGCCCC  
TGAACCATATATTGTTATCACTGGATTGAAAGTCACCGTTATCTTATTTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTTNTTGCCGAC

0978192.101501



## FIGURE 72

CAGCCCCGCGCGCCGGCCGAGTGGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCGCCGTGGGCATGGGCGCACTGGCCCCGGCGCTGCTGCTGC  
CTCTGCTGGCCAGTGGCTCCTGCGCGCCGCCCGGAGCTGGCCCCGCGCCCTTACGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCACCCCGGGACCCGGACCCC  
TGCCGAGCGCCACGCGACGGCTTGGCGCTCGCCCTGGAGCCTGCGCTGGCGTCCCCGCGG  
GCGCCGCCAATTCCTTGGCCATGGTAGACAACCTGCAGGGGGAAGCTTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACCTTTCGCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT  
CTAGCACATACCGCTCCAAGGGCTTTGACGTACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTGTCAA  
CATTTGCCACTATTTTTGAATCAGAGAATTTCTTTTGGCTGGGATTAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAGGAGACATCTGTGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCG  
AAATTGAAATTTGGAGGCCAAAGCCTTAATCTGGAAGTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCTGCGCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCAGAAATCTCTGATGGTTTCTGGAAGTGGTCCCAG  
CTGGCGTGTGGACGAATTCGGAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTACG  
CCATGATGGGGGCCGGCTGAATTATGAATGTTACCGATTGCGCATTTCCCATCCACAAT  
GCGCTGGTGATCGGTGCCACGGTGTGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA  
GAGGTGGGCTTCGACGCGAGCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGATTGTGTCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT  
AATCGTCTGTCTGCTGCGGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTGCTCA  
ATGATGAGTCTCTCTGGTCAGACATCGCTGGAATGAATAGCCAGGCTGACCTCAAGCAA  
CCATGAACCTCAGTATTAAGAAATACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCTGTGCCCAACCCGTCTTCAATCTCTGTTCTGCTCCAGATGCCTTCTAGATTAC  
TGTCTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA  
AAAAAAACTTCATTCTAA

09973192-101501

## FIGURE 73

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493

><subunit 1 of 1, 518 aa, 1 stop

><MW: 56180, pI: 5.08, NX(S/T): 2

MGALARALLLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGPGPPTAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGDSEGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSSTYRSKGFDTVKYTQGSWTGFGEDLVTIPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDIIWYTPIKEEWYYQIEILKLEIGGQSLNLDCREYNADKAIVDSGTTLLR  
LPQKVFDVAVEAVARASLIPEFSDGFWTGSQACWTNSETPWSYFPKISITLRDENSSRSFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAAGAVSEISGPFSTEDVASNCVPAQSLSEPIWIVSYALMSVCGAILLVLLVLLLPFRCL  
QRRPRDPEVVNDESSLVRHRWK

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Transmembrane domain:**

amino acids 466-494

#### **N-glycosylation sites.**

amino acids 170-173 and 366-369

#### **Leucine zipper pattern.**

amino acids 10-31 and 197-118

#### **Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

09978192-101501

# FIGURE 74

CGCCTCCGCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
 GCAGCCGCTTGGCGGCGATCCAGGGCGGTGCGGGGCTGGGCGGAGCCGGGAGGCGCGGCC  
 GGCATGGAGGCGCTGCTGCTGGGCGCGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
 CAACCTGGTGAAGGCCCCCGCTGCGGCGGCATGGGCAACCTGCGGGGCGGCACGGCCGTGG  
 TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGAGCG  
 CGCGTGGTGTGGCTGCCGAGCCAGGAGCGCGGGGAGGCGGCTGCCCTCGACCTCCGCCA  
 GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
 GGGCCTTTGCCACTGCCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
 GGTATCAGTTCTGTGGCCGAGCCCGTGAGGCGTTTAAACCTGCTGCTTCGGGTGAACCATAT  
 CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCCTTGCTGAAGGCATGTGCCCTAGCCGCG  
 TGTGTGGTGGTAGCCTCAGCTGCCACTGTGCGGGACGCTTGTGACTTCAAACGCTTGGACCGC  
 CCAGTGGTGGGCTGGCGGCGAGGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
 GTTTGCCCGGGAGCTCGCCAACAGCTTGAGGCCACTGGCGTCACTGCTATGACGCCACCC  
 CAGGGCCTTGGAACCTCGAGCTGTTCTGCGCCATGTTCTTGATGGCTGCGCCCACTTTTG  
 CGCCCATTTGGCTTGGCTGGTGCTCCGGGCACCAAGAGGGGGTGCCAGACACCCCTGTATTG  
 TGCTCTACAAGAGGCGATCGAGCCCTCAGTGGGAGATATTTTGCCAACCTGCCATGTGGAAG  
 AGGTGCCTCCAGCTGCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
 CTGGCAGGGCTTGGGCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
 AGAGGCCCCATCTTCTCTAAGCACCCCCACCCTGAGGAGCCACAGTTTCTCAACCTTACC  
 CCAGCCCTCAGAGCTCACCAGATTGTCTAAGATGACGCACCGAATTGAGCTAAAGTTGAG  
 CCTGAGATCCAGCTCTCTTAACCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCTTT  
 GAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
 CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT  
 AATGGGTGATTATTTCTTCTGAGAGTGACAGTAACCCAGATGGAGAGATAGGGGTATGCT  
 AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG  
 ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
 TGAATGATCCCTTTGCAACCGCTCTAGCTAGGTAGTTAAATTACCCCATGTTAATGAAGCG  
 GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCAGTGAAGTAGGGTGTGAGAAGTGA  
 GTCAGGGCAGGGCAGCTGTGATCGAGGTGCCCATGGGAGTAAGGGGACGCCCTTCCGGGCGG  
 ATGACGGCTGGGGTCATCTGTATCTGAAGCCCTCGGAATAAAGCGGTTGACCGCCAAAA  
 AAAAAAAAAAAAAAAAAA

06978192.101501

## FIGURE 75

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANSIGIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLSSEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHTLLLPCLKACAPSRVVVVASAAHCRGRDLDFKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPGVNSELFRLRHVPGWLRPLLR  
PLAWLVLRAPRGGAGTPLYCALQEGIEPLSGRYFANCHVEEVPPAARDDRAAHLWEASKRL  
AGLGPGEDAEPEDEDPQSEDEAPSSLSTPHPEPTVSPQYPSPQSSPDLSKMTTHRIQAKVEP  
EIQLS

**Important features:**

**Signal peptide:**

amino acids 1-16

**Glycosaminoglycan attachment site.**

amino acids 46-49

**Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

00978192-101504

# FIGURE 76

GGAGGAGACAGCCTCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATC**ATG**GGAGGCATGGCTCAG  
 GACTCCCCCGCCAGATCTCTAGTTCACCCCCAGGACAGCTGTTTCAGGGCCCTTGCCCTGCGAGGATGAGCTGC  
 CAAGCTCTCAGGCCAGCCACCTCCACCATCCGCTGGTTGCTGAATGGGCAGCCCTTCCAGGATGGTGCCCGACAC  
 CCACACCACTCTCTGCCTGATGGGACCCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCCCAGATGGCCAG  
 GCCCTGTCCACAGACTCTGGGTGCTTACACATGTGAGGGCCAGCAACCGGCTTGGCAGCGGAGTCCAGCAGAGGGGCT  
 CGGCTGTCTGGGCTGTCTCTCGGGAGGATTTCCAGATCCAGCCTCGGACATAGTGGGCTGTGGTGGGTGAGCAG  
 TTTACTCTGGAATGTGGGCGCCTTGGGGCCACCCAGAGCCCAAGCTCTCATGTGGGAAGATGGGAAACCCCTTG  
 GCCTTCAGCCCGGAAGGACACAGTGTCTCGGGGGGTCCTGCTGATGGCAGAGCAGAGAAGAGTGACGAAGGG  
 ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGAGCCCGGGTTTCCATTCAGGAGCCC  
 CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTTCAGCTGGAAAAATGTGACACTGTCTGTAACCCGGAT  
 CCTGTAGAGGGCCCCAAGCGTAGACCCGGGTGTGGCTCAGCTGGAAAGTTCAGTGGCCCTGTGCGCTGCCCAA  
 TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCGGGAGGCGCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC  
 GGCTGGCAGAGCGCAGAGCTTGGAGGCCCTCCACTTGGGGCCAAAGACTACGAGTTCAAAGTGAGACCATCTCTTGGC  
 CGGGCTCGAGGCCCTGACAGCAACGTGCTGCTCTGAGGCTGCCGGAAGTGGCCAGTGCCCCACCTCAGGAA  
 GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCACACCTGCTGTGAAACACACAATGGCATC  
 ATCCGTGGCTACCAAGTCTGGAGCCTGGGCAACACATCACTGCCACCAAGCACTGGAGCTGTAGTTGGTGAGCAG  
 ACCCAGCTGGAATCGCCACCCATATGCAGGCTCTACTCGTGAAGTGGCTCCAGTCACTGGTGTGGTGTGGAGT  
 GGGGAGCCCAAGTAGTACTGTCTGCCCTCTTTTAGAGCAGGCCATGGAGGAGCCACCCAAAGAAACCCAGTGAGCAT  
 GGTCCCTGGACCTGGAGCAGCTGGAGGCTACTTTGAAGCGGCTGAGGTCACTGGCACTCGGCTGTGACAT  
 TGGCTGTGCTCTTGGGCACCGCCCTGTGTATCCACCGCGGGCGGAGCTAGGGTGACCTGGGCCAGGTTGTG  
 TACAGATTAACAGTGAGGATGGCACTCTTAAACACAGGATGGATCAAGTGACTCCAGTGGTTTGGCAGCACT  
 TGGCTTCCACCTCTTGGCTCTCGGGACCTGAGCAGCAGCAGCAGCTCAGCAGTCCGCTGGGGCGGACATCCCGG  
 GACCCTAGACTGTCTGCTCCTTGTCTCTCTGGGACTCCGAAGCCCGGGGCTGCCCTTCCAGCAAC  
 AGCACTTTTATGGCTCCTCTCATCGCTGAGCTGCGCTCCAGTACCCAGCCAGGCGCAAGTCCCAGGTCCAGCT  
 GTACGCTGCTCCCAACCCAGCTGGGCCAGCTCTCCAGCCCTGTCTCAGCTCAGACAGCTCTTGCAGCGCCAGG  
 GGACTCTCTCTCCCGCTGTCTCTTGGCCCCGAGAGGCTTGGAAAGCCAAAGAGCCAGGAGCTTCAGCAT  
 GCCAACAGTTTCCCACTGCTCCGGGGCAGGCCATCTCTGGAGCTCCGGGCTCTGTGAGTTGGGAATAGAGGTTCC  
 AAGAATCTTTCCCAAGCCAGGAGCTGTGCCCAAGCTCTGGTTGCTCTGGCGGGCCCTTGGAGCCGAATCTCTC  
 AGCTCCTCAAATGAGCTGGTTAGTCGTATCTCCCTCCAGCAGCCCTCTTTCTCATGAACTCCCCCACTCAG  
 AGTCAACAGACCCAGCTCCGGTGGCACCACAGGCTCCCTCCATCTGCTGCGCAGCAGGCCCATCCCCATC  
 CTTAGCCCCCTGCACTCCCCCTAGCCCCCAGGCTCTTCCCTCTTGGCCCCAGCCAGCTTCCAGTGGCTGTCC  
 AGCTCTCTCACTGTATCCCTGGGGGAGGATCAAGACAGCTGCTGACCCCTGAGGAGGTAGCCCTGTGTTTGGAA  
 CTCAGTGAGGCTGAGGAGACTTCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCTTCAACCCCCACCACTAT  
 GGGTACATCAGCTGCCAACAGCTCAGAGTTACGGACATGGCAGGACTGGAGGAGGGGTGGGGGCCAAGGGG  
 GGAGTCTGTGTGCCCACTCTGGCCCTGCTCAACCCCAACCCAGCGAGGGCTCTTAGCCAATGGTTGGGGC  
 TCAGCTCTGAGGACAAATCGGCCAGCGCCAGAGCCAGCTTGTGAGCTCTCCGATGGCTCTCTCTCTGCTGAT  
 GCTCACTTGTCCCGGGCTCTGGCAGTGGCTTGGATAGCTTTGGTTTCCGTCTAGAGCCCGAGGAGCGCAGACTGC  
 TGGGATGGAGGCCAGACTGGTTGGAAAGCATGGAGGTCAAGCACCCAGCGCTGGGAAGGGGGATGCCCTCC  
 TGGCCCCCTGACTCTCAGACTCTCTCCAGAGAAGTCACTCTGCTGCTGATGCCAGGCTGTGCTCTCTCTCT  
 GTAGATTACTCT**GAA**ACCGTGTCTCTGAGACTTCCAGACGGGAATCAGAACCACTTCTCTGTCCACCCACAAG  
 ACCTGGGCTGTGTGTGTGGTCTTGGCTGTGTTTCTGTGAGCTGGGTCCACTTCCCAAGCTCCAGAGCTCAGAGC  
 TTCTCCCTCCACAGTTGTGAAAAACAAATGAAACAAATTAGAGCAAGCTGACCTGGAGCCCTCAGGAGAGCAAA  
 ACATACCTCCACCTGACTCTTAGCCACTGCTTTCTCTCTGTGTCATCCACTCCACCCAGAGTTTGTGGC  
 CTGAGGAGCAGCCCTGCTGTGCTCTTCCCCACATTTGGATCAGAGGAATGGAGGAGCCAGAGGTGCTCTT  
 GTGGAGCAGCAGTGGCTCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGAGAGCCCTCTCAGCTTACTCT  
 GGGCCCCCTCTCTAGAGAGAGCTCAACTCTCTCCCACTCACCATTGGGAAGAAATAATTAATGAATGCCACTG  
 AGGCATCTGAGGCCCTACTCTCACTCAACAAAGGGTTCAAGGCTGGGTCTAGCAGGATCTGTGAAGGAGGGAGG  
 TATGAGACCTGAGGTCAAAGCACCATCTCGTACTGTTGTCACTATGAGCTTAAAGAAATTTGATACCATAAAT  
 GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## **FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404  
<subunit 1 of 1, 985 aa, 1 stop  
<MW: 105336, pI: 6.55, NX(S/T): 7  
MGGMAQDSPPPQILVHPQDQLFQGGPGPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHLLLP  
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAESDEGTYMCV  
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENVTLINPDPAEGPKPRPAVWLSWKV  
SGPAAPAQSYTALFRQTQATPGGQCAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLRLPEKVPSPAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNLTLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGPW  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST  
FYGSLIAELPSSPTPARPSPQVPAVRRLPPQLAQLSSPCSSDSLCSRRLSSPRLSLAPAEA  
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS  
SSNELVTRHLPAPLFPFHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS  
LSGSPASSRLSSSSSLSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPPRPCLTPTPSEGLANGWSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLFEPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHRTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPDVYS

### **Important features:**

#### **Transmembrane domain:**

amino acids 448-467

#### **N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

#### **N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

#### **Phosphotyrosine interaction domain proteins**

amino acids 740-753

09370362.101501

## FIGURE 78

CTCCCACGGTGTCCAGCGCCAGAAATGCGGCTTCTGGTCTGCTATGGGGTGCCTGCTGCT  
CCCAGGTTATGAAGCCCTGGAGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGTT  
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
GGGATCCTCTTCTCTCGTGTCTTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGTCTATTGTGACCCCTGTGGA  
ACCTCACCCCTCAAGACGCTGGGAGTACTGGTGTGGGTCGAAAAACGGGGCCCGATGAG  
TCTTTACTGATCTCTCTGTTCTCTTTCCAGGACCTGCTGTCCTCCTCCCCCTCTCCAC  
CTTCCAGCCTCTGGCTACAACAGCCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCAGCCCC  
CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACACAGCCCAAGCAGGGGAAGACAGGG  
GCTGAGGCCCCCTCCATTGGCCAGGGACTTCCAGTACGGGCACGAAAGGACTTCTCAGTACAC  
AGGAACCTCTCTCCTCACCAGCGACCTCTCTCCTGCAGGGAGCTCCCGCCCCCATGCAAG  
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGTGCTGAGCCTTCTGTGAGC  
CGCAGGCTGATCGCCTTCTGCAGCCACCTGCTCTGTGGAGAAAGGAAGCTCAACAGGCCA  
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCTTGACTGCGGAGGAAAAGGAAGCC  
CCTTCCCAGGCCCCCTGAGGGGGACGTGATCTCGATGCCTCCCTCCACACATCTGAGGAGGA  
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCTGGCCAGGCCAGCAGT  
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCACACTCAGCCTCAGAG  
TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCGAGGCTCTCCTCTGTCATGTTCCA  
GCTGACCTAGAAGCGTTTGTGAGCCCTGGAGCCAGAGCGGTGGCCCTTGTCTTTCGGGCTG  
GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCTCA  
GCAGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCTGGGC  
CTCATGCCCAGTGTGCGACCTGCTCTCTCCACTCCAGACCCACCTTGTCTTCCCTCCC  
TGGCGTCTCAGACTTAGTCCCACGGTCTCTGTCATCAGCTGGTGTATGAAGAGGAGCATGCT  
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACTGCATCCAGCCCTCAGGAAGCCT  
GTGAAAAACGTGATTCTTGCCCCCACCAGACCCACCAAAACCATCTCTGGGCTTGGTGAC  
GACTCTGAATTTTAAACAATGCCCCAGTGACTGTGCATCTGAGTTTGAAGGCCAGTGGGCCCTG  
ATGAACGCTCACACCCCTTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGCTTCCACCTGCCC  
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGAATCCCTCAGAGCCTGCTAAG  
TCCAGGCCCTTGGTCAAGTCAAGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG  
TTGCCCTTNNCCATTTGCCCTCCCCTGNNCCATGCTTCTTGGCTTTGGAATAATGATGAAGA  
AAACCTTGGCTCCTTCTGTCTGGAAGGGTTACTTGCATTTGGGTTCTGGTGTAGAGA  
GAAAAGTAGAAAACAGAGTGCACGTAGGTGCTAACACAGAGGAGAGTAGGAACAGGGCGG  
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGCGGGGTGGTGGTAAAGTA  
GCACAACACTATTTTTTTCTTTTCCATTATTGTTTTTAAAGACAGAATCTCGTGCT  
GCTGCCCAGGCTGGAGTGCAGTGGCAGATCTGCAAACTCGCCTCTGGGTTCAAGTGATT  
CTTCTGCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACCTGGCTAATT  
TTTGACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCTGAC  
CTCAAATGAGCCTCCTGCTTCACTCTCCAAATTTGCCGGGATACAGGCATGAGCCACTGTG  
TCTGGCCCTATTTCTTTAAAAAGTGAAATTAAGAGTTGTTACAGTATGCAAACTTGGAAAG  
ATGGAGGAGAAAAAGAAAAAGAAAAAATGTACCCCATAGTCTCACCAGAGACTATCAT  
TATTTCTGTTTGTGTTACTTCTTCCACTCTTTTCTTCTTCACTAATTTTCCGGGTGTTCTT  
TTTACAGACAATTATCTGTATATACAACCTTTGTATCTGCTTTTCCACTTCTGCTTCTGCTC  
ATCACTTTATTCAGCACTTCTCTGTGTTTTACAGACCTTTTTATAAATAAAATGTTTCATCA  
GCTGCATAAAAAAAAAAAAA

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## FIGURE 79

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALGPEEISGFEGDTVSLQCTYREELRDHRKYWCRKGILFSRCS  
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCQVEKRGPDSELLISLFV  
FPGPCCPPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSI PMVRI  
LAPVLVLLSLLSAGLIAFCSHLLLRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD  
VISMPPLHTSEELGFSKFVSA

### **Important features:**

#### **Signal peptide:**

amino acids 1-17

#### **Transmembrane domain:**

amino acids 248-269

#### **N-glycosylation site.**

amino acids 96-99

#### **Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

#### **Ig like V-type domain:**

amino acids 13-128

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## FIGURE 80

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAAGTGCCTGTATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGCCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACCTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATACCGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCAGATCAACAGCCGGAGGTGGTGCAGCAACCTCACCCCGAACGTCCC CAAC  
GTGTGCCCGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCAAGAGCCTCAGGGTCTGGGTTACTGGGAGGCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTCTTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

0978192.101501

## FIGURE 81

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCNLTNPVNPVNCMYCSDLNPNLKDITVICAMKITQEPQGLGY  
WEAWRHHCQGKDLTEWVDGCD

### **Important features:**

#### **Signal peptide:**

amino acids 1-18

#### **N-myristoylation site.**

amino acids 67-72

#### **Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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## FIGURE 82

AGCCGCTGCCCCGGGCCGGGGCGCCCGCGCGCGCACCATGAGTCCCCGCTCGTGCCTGCGTTC  
GCTGCGCCTCCTCGTCTTCGCGCTTCTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTCGTCGGTGGGGAGCATCTCAGAGGAGGAGAGCTGCGAGAAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGCGCTGGAACTGCTCCACAC  
TCGACTCCTTGCCCGCTTTCGCGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCCTTCGTG  
TACGCCATCTCTTCGCGAGGTGTGGCCTTTGTCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGCATGGGGTCAAGCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCAGAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGCCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACATGAGGCCGGCAG  
GAAGGCCATCTGACACACATGCGGGTGGAAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG  
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTACGCACTGAAGGAG  
AAGTTTGATGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGCGTGTGGGCAAGAGGGGCGGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAAATCCACTGGTGTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGGAGTTGCACAGTGCCGATGACCGCCTGCGCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCAGGGAAGGCCGATAATTTAAACAGTCTCCACCACCTACCCCAAGA  
GATACTGGTTGTATTTTTTTGTTCTGGTTTGGTTTTTGGGTCTCATGTATTATTATGCGGAA  
ACCAGGCAGGCAACCCCAAGGCCACCAACAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT  
GCCACTGACCAAAAGGGACCTTGCTCGTGC CGCTGGCTGCCCGCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGACAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCAACCCCTCTGGA AAAAAGAACTCTTA ACTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAAGG  
GAACAAGCAGATACCAGGTCAAGGGCACCAGGTTCAATTCAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCACCCCTAGAAACCGACCTGCCCCAGCCTGCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTTAGGCAGGCATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCGAGTCACCTTTTACAGCGCTGTTCTCCTCATGAAACTGAAAAACACACAC  
ACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCTTTGTCAGTCATGCCCGAGTCACCTTTTACAGCACTGTTCTCTC

0978192-101501

## **FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEETCEKLKGLIQRQVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLVPFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCDNIAYGVAFSQSFVDVREERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSEVKTWCWRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCFKHWCCFVKCRQCQRLVELHTCR

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 88-91 and 297-300

#### **Wnt-1 family signature.**

amino acids 206-215

#### **Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

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# FIGURE 84

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCTTGGTC  
ACCACAGTCTCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGCGCTGG  
GTGCCCTGAAGGAGGAGGTTCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTGAGGGCTACCACTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGGCACTGGAACCAGGGAGAGGCCAATGACGCTTGGGGCGCGAGAAGTGTGTATGATGC  
TGACACAGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAAGTGTGACCCCGCCCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCTGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACTAAC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAAGTGA  
AGCTGTTTTTGACGCTGAGGAAGCATCAATAAATATTGAGAAATGAAAAA

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## **FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352  
<subunit 1 of 1, 293 aa, 1 stop  
<MW: 32562, pI: 6.53, NX(S/T): 2  
MDTRYSKWGSSEEVPGGPWGRVHWSRRPLFLALAVLVTTLWAVILSILLSKASTERAA  
LLDGHDLRLTNASKQTAALGALKEEVGDCHSCSGTQAQLQTTRAEELGEAQAKLMEQESALR  
ELRERVQTQGLAEAGRGREDVRTELFRALAVRLQNNSCPEPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVLSLSFS  
HWNQGEFNDAGRENCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 31-54

#### **N-glycosylation sites.**

amino acids 73-76 and 159-162

#### **Leucine zipper pattern.**

amino acids 102-123

#### **N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

#### **C-type lectin domain signature.**

amino acids 264-287

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## FIGURE 86

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCTTTCTCCCACGTCCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTTGGCCGGCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGTGTCTCTGTCCGGGTGATGGAAACCCAGCCCGCGCCGCCCTGGGCAAG  
GCCCTCTGCCTCTCCTCTGGCCACTCTCGCGCGCCGGGCCAGCCTCTTGGGGGAGAGTCT  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCTGTTCGGCCCCCTCGCGAGTGGTCTTCGTGTCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAAGTAAACGGGCTGCG  
CGACTTTGCGGAGCGCGCGCAGGCCTGGGCGCTGATGAAGGAGATCGAGGCGCGGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTTCGGCGCCCGCGCTCCCCAGCGGCACCGGGCAGACG  
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCATCGTGCC  
CAGCCCCGACTGGTTCTGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGACCGTTGGCGGG  
AACAGGCGCGCTGGACCTGTACCCCTACGACGCCGGGACGACAGCGGCTTCACCTTCTCC  
TCCCCAACTTCGCCACCATCCCCGAGGACACGTGACCGAGATAACGTCTCTCTCCAG  
CCACCCGGCCAACTCCTTCTACTACCCGCGGTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCTGCCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTCTCTCTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGCTACGTCCGGTCCAGCCCGCCAAACACGGGAGCCCTGCCCGAGCTCGAAGAAGAG  
GCTGAGTGCCTCCCTGATAACTGCGCTTAAGACCAGAGCCCCGACGCCCTGGGGCCCCCG  
GAGCCATGGGGTGTGCGGGGCTCCTGTGCAGGCTCATGCTGCAGCGCGCCGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
CTGTTGGCCGGCAGCGGCATTGGGAAACAGCCTCCTCCTTCCCAACCTTGCTTCTTAGGGG  
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGTCCAGGAGATTGTCTTTCATCG  
TCCAGGGGCTGGCTCCACGCTGGTTGCAGATACCTCAGACCTGGTGTCTTAGGCTGTGCTG  
AGCCCACTCTCCCGAGGGCGCATCAAGCGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

0978192.101501

## FIGURE 87

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFABERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVSPDWFVGVDSLDLCDGDRWREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP  
RAFIPPAFVLPSPRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRIGTKSRTRYVRVQPA  
NNGSPCPELEEEAECPVDNCV

**Important features:**

**Signal peptide:**

amino acids 1-26

0970132.103501



## FIGURE 88

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTGTTGGTGTCCCTGTCTTGCGTGA  
TATTGACAAACTGAAGCTTTCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA  
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCACGAATGGGAAGGTTTTATTGAAACTA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT  
ATCCAACITTTGTTTGGAAAGCTTATTATGACAATACCATTTTTTATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTTCATTACGGTTGCGTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACTCGGGTCGAGCAGATGAACT  
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCATAATCCACACAAAAATAAAAGCTGT  
GAGGTTTTGTTTAAATCCTTTTGATGACATCATTCCAAGGGAAATTAAGGCTGAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAATTTTAGTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAAGTAGTCAGCTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TGTAGAAAGTGAAAAGGTGATGCACCAGATTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAA  
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAACGGGAACCTTAGCAG  
CAAAACAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAGAAGTGAAGAGGAAGAA  
GCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAACTTCCCGGAAGATCAGACCCTTGCACTGCTGAACAGT  
TTAAATCTAAACTCACTCAAGCAATTGCTGAAACACCTGAAAAATGACATTCCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTACATGTACTTCAGTTTGAGGATAAAAGCAGAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAGAAGGAGGGAAGAAAGCAAAAGCTGATGAGAGAGAAAAAGAAAGAAGATAAAT  
GAGAAATATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTGAACCTGTTGTCTGGTTTGG  
AAAAACAATTATCTTGTTTTGCACAAATTGTGGAATGATGTAAAGCAATGCTTTTGGTTACTGG  
TACATGTGTTTTTCTTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCT  
TCCACAAAAA

0978192.101501

## FIGURE 89

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919

><subunit 1 of 1, 472 aa, 1 stop

><MW: 53847, pI: 5.75, NX(S/T): 2

MSNIYIQEPPTINGKVLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFNPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGTKNFSLLSFGEEAEIEEEVNRVSQSMKGKSKSSHDLKDDPHLSSVPV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKCLKDTSANVKSAGEGEVEKESV  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEAEPPDGAVAERYRREKQKYEALRK  
QQSKKGTSRDQTLALLNQFKSLTQAIATPENDIPETEVEDEDEGWMShVLQFEDKSRKVK  
DASMQSDTTFEIIDPRNPVNRKRREESKKLMREKKERR

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **N-glycosylation sites.**

amino acids 109-112 and 201-204

#### **Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

#### **Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

09978192.101501

## FIGURE 90

CGCCGCGTGTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG  
CCCGCCTCGGCTTTTGAGGCGAGAGAAGTGTCCAGACCCATTTCGCCTTGCTGACGGCGTGC  
AGCCCTGGCCAGACATGTGCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC  
GTGGCCGCGCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA  
CCCTTCTGTGGGGCTCAATTTTGGAATCTTGGAAGTACTTCAACTCCAGCACTACATCTGC  
CTCCTTCAAGTGGTTTTTGGAAACCGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
GGAGGAACAAATACAGGTGCCCTTGCAACCAAGAGGCTCAAGTGGTCAACCAATATGGAAC  
CCTGCAAGGAAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCTT  
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAA  
GGAATCAGAGATGTACACCTACCCGCTTGGATGGAGTCTCGCTCTGTGCCAGGCTGGAG  
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCTCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCTGGGGCCAGCTGGCCCTCG  
ATGTACGTGACGACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT  
GAACGTGTACGCGCGCGGCGCGCCCGGGATCCCCAGCTGCCAGTGTATGGTCTGGTTCC  
CGGGAGGCGCTTCTATCTGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC  
GAGAAAGTGGTGTGTTCTCTGCAGCACAGGCTCGGCATCTTCGGCTTCTGAGCACGGA  
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACAGATGGCGGCTCTGCGCTGGGTGC  
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCCTGTTCCGCCAGTGGCG  
GGGCGCATGAGCATCTCAGGACTGATGATGTCAACCCTAGCCTCGGCTCTCTCCATCGGGC  
CATTTCCAGAGTGGCACCGCGTTATTAGACTTTTCTACTAGTAACCCACTGAAAGTGG  
CCAAGAAGGTTGCCACCTGGCTGGATGCAACCACAACAGCACACAGATCTGGTAAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGCCAACAGATGAGATTCTCCAACT  
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCAGATGACCTTTGGTGTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAACTTGAATTCATTTGGCTCTTGCCCTTATAATATCACAAGGAGCAGGT  
ACCACTTGTGGTGGAGGAGTACTTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC  
TACCACGAGAAACCCCAATGATGGGAATCTGCCCTGCTGCCACGCTACAACAAGGATGAA  
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCACTGAAGCTCAAGGAGAAGAAGATGGC  
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCACCATTCCAGGCCCTGGGGAGACTAGCCA  
TGGACATACCTGGGGAACAAGATTCTACCCACCCAGTTTAGAACTGCAGGAGCTCCCTGCT  
GCCCTCCAGGCCAAAGCTAGAGCTTTTGCCCTGTTGTGGGACCTGCAGTCCCTTTCCAGCC  
TGACATCCCATGATGCCCTCTACTTCACTGTTGACATCCAGTTAGGCGCAGGCCCTGTCAAC  
ACCACACTGTGCTCAGCTCTCCAGCTCAGGACAACCTCTTTTTCCCTTTCTCAAATCCT  
CCCAACCTTCAATGTCTCCTTTGTGACTCCTTCTTATGGGAGTGCAGCCAGACTGCCACTGC  
CCCTGTCACTGCACCCAGCTTGGCATTACCATCCATCCTGTCAACCTTGTTCCTGTCTGT  
TCACATGGGCTGGAGGCTAGGGCAGGTTGTGACATGGAGCAAACTTTGGTAGTTTGGGA  
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG  
TCTCTTCAATAAAGAGTGTGATTAGAAAAA

09978192.101501

## FIGURE 91

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAFSSG  
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTQGGKQMHVGTPIQVFLGVFPFSRPP  
LGILRFAPPEPPEPWKGIRDATYPPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVIYAPARAPGDPQLPVMVWFFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLDQMAALRWVQENIA  
AFGGDPGNVTFLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCLRALSGTKVMRVSNNKMRFLQLNFORDP EEIIWSMSPVVDGVVIPDD  
PLVLLTQGVSSVPYLLGVNNLEFNWLLFPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD  
IVQDATFVYATLQTAHYHRET PMMGICPAGHATTRMKSTCSWILPQEW A

**Important features:**

**Signal peptide:**

amino acids 1-29

**Carboxylesterases type-B serine active site.**

amino acids 312-327

**Carboxylesterases type-B signature 2.**

amino acids 218-228

**N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

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1000

GAGAACAGGCCCTGCTCTCAGGCAGGCCCTGCGCCTCCTATGCGGAGATGCTACTGCCACTGCTGCTGCTCTCGCTGCTGGCGGGGCTCCAGAGCTATGATGGGAGATCTTGATACAGTGCAGGAGATCAGTATGATGTGCGGGAGGCGCTGTGACCTCTGTGCGCTGCTCTTTCTCTCACCCCGACAAGACTGGACAGGGTCTACCCCAAGCTATGTGCTATGTTTCAAAGCAGTGACTGAGACAAACAAGGGTGCTCTCTGTGGCCACAAAGCCACCAAGAGTCGAGAGGTGGAATGAGCACCGGGGCCGATTTCAGCTCACTGGGATCCCGCGAAGGGGAAGTCTCTTGGTGATCAGAGACGCGCAGATGCAGGATGAGTCAAGTACTCTTTCCGGTGGAGAGGAAGTATGTGACATATAATTTTCATGAACGATAGGGTTCTTTCTTAAAGTAACAGTGTACAGTTACGCCACAGCCCAAGGACCACAACACCGACTCTCACTGCCATGTGGACTTCTCCAGAAAGGGTGTGAGCGCACAGAGGACCGTCCGCACTCCGTGTGGGCTATGCCCGCCAGAGACCTGTTATGACGATTTTCAGTGCACAAACGCCGCGCTGGAGGCCCAAGCCAGGGAATGTCCATAGCTGGAAGGCCAAAGAGCCAGTTCTCTGCGGCTCTCTGTGCTGTGACAGCCAGCCCCCTGCCACACTGAGCTGGGTCTGTGCAAGACAGATCTCTCTCGTCCCTACCTGGGGCCCTAGACCCCTGGGCGTGGAGCTGCCCGGAAAGGTGGGATTCAGGGCGCTACACTGCGAGCGAGAAACAGGCTTGGCTCCAGCAGCGAGCCCTCTCTGTGTCAGTATCTCTCCACAGAACTCCAGAGTGTAGTTTCCCAAAGCAACAGCAGCTCTGTGAAACCTTGGGAACGGCAGCTCTCTCCAGTACTGGAGGGCCAAAGCCTGTGCTGGTCTGTGTACACACAGCAGCCCCCGAGCAGGCTGAGCTGAGTCCAGGAGGGACAGGTTCCGAGAGCCCTCCGAGCCCTTCGAGCCCGGGGTCTGTGAGCTGCTCCGGTTCAAGTGGAGCAGGAAGGAGAGTTCACTGCCAGCTCGGCACCCACTGGGCTCCGAGCAGTCTCTCTCAGCCTCTCCGTGCACTAAGAAAGGACATCATCAACGGCATTTCCAAAGCGGAGCGTTTCTGGGAATCGGCATCAAGCTCTTTCTTTCTGCTGCGCTGATCATCATGAAGATTCTACCGAAGACGCACTCAGACAGAAACCCGAGGCCAGGTTCTCCCGGCACAGCACGATCTCGATTACATCAATGTGGTCCGACAGCGCTGGCCCTGGCTCAGAAAGCGGAATCAGAAGGCCAACCAACAGCTCTCGGACCCCTCTCCACAGGTGCTCCTCCCGAAGATCAAAAGAAACCAGAAAAAGCAGTATCAGTTGCCAGTTTCCAGAAACCAAATCACTCAACTCAAGCCCCAGATCCGAGAGGCCAAGAGGAGCTCATATTGCCACGCTCACTTCCAGGGCTCAGACCCAGGCTGAGGCCGAGTGCCAAGGGCACCCAGGCGGATTATGCAAGTCAAGTTCCAATGAGGGTCTCTTAGGCTTTAGGACTGGGACTTCGGTCTAGGGAGGAAGTAGATGAAGGTTGAAGATAACAGATGCAAAGTTCTTTTAAAAAAACATCTGGCCAGGGCACAGTGGCTCAGCCTGTATCTCCAGCACTTTGGGAGGTTGAGGTGGCGAGATCGCTGAGGTGGGAGTTTCGAGACAGCCCTGCCAATCTGGTGAACCCCGCTCTCATATAAAATACAAAAATAGCTGGGCATGTGGGAGCGCCTGTAACTGACTCTACTCTTGGGAAGCTGAGGCAGGAAGTCACTGAACCTGGGAGACGGAGGTTGCACTGAGCCAAGATCAACACTTGCCAGCAGCTGGGCAACAAGCGAGACTTCACTTCAAAAAAAATCTTCAAAATGGGTGGGTGTCTGTAATCCAGCACCTTTGGGAGGCTAAGGTTGGGTGATGTTGCTTGAAGCCAGGAGTTCGAGACAGCAGCTGGGCAACATGGTGAACCTGATCTCTGAACAAAATACAAACATAGCTGGGCTTGGTGTGTGTGCTGTAGTCCAGCTGTCAGACATTTAAACAGAGCAACTCCATCTGGAATAGGAGCTGAATAAAATGAGGCTGAGACCTACTGGGCTGCATTTCCAGACAGTGGAGGCACTTAAGTCAACAGGATGAGACAGGAGTCCTACAAGATACAGGTCATAAAGACTTGTGATAAAACAGATTGCAGTAAAGAAGCCAACCAATCCACCAACAAACCAAGTTGGCCAGAGATGACCTGTGGCTCTCTCACTGTCACTCTCCAGCAGCACTGACATTTCAAAATGCCATGGCAACCTCAGGAAGTTACCGGATATGTGCCCAAAAGGGGGAGGAATGAATAATCCACCCCTTGTTTAGCAAATAAGCAAGAAATAACCATAAAAATGGGCAACAGCAGCTCTAGGCGCTCTCTGTCTATGAGTAGGCCATTTCTTTGCTCTTTCTTTCTTAATAAGTTGCTTTCTCTCTTAAAAAA

## **FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002

><subunit 1 of 1, 544 aa, 1 stop

><MW: 60268, pI: 9.53, NX(S/T): 3

MLLP LLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSFSYPRQDWTGSTPAYGYWFK  
AVTETTKGAPVATNHQSREVE MSTRGRFQLTGDPKAGNC SLVIRDAQMQDESQYFFRVERGS  
YVTYNFMNDGFFLKVTIVLSFTPRPQDHNTDLTCHVD FSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCRAENRLGSGQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKNQKATPNSRPTPPPPGAPSPESKKNQKKQYQLPSFPPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

**Important features:**

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins  
signature.**

amino acids 365-371

00973557-10501

## FIGURE 94

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAAGTGTATTATTACTGCTGCGTTT  
TATGTTGGGAATTTCTCTCCATTAGGCCTTGTCTTGGAGCAACAGAAAACTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGGCATCTCATTTGAGAGTGAAGCGTGGCTGGTGTGGAACCAATT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCAGTATCGGCCAGCTAAGATCTGATTTAGA  
CAATGGAAACAAATCTTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAAGACAGGTGACATATATGCCATACAGAACTTGTATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTGCATCAAAGTTTCGGATATCAATGACAATGAACCAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTTATCCAGGTGACAGCAAGTGTAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGTATTAAATTAACCTTTTCAGATGTTAATGACAATAAGCCATATATTTAA  
AGAAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGATTGAAGAGGAT  
GATTCGCAACACTTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTTATATTAA  
AAAGAAGTGGATTTTGGACACCAGAACCACACGGTATTTAGAGCAAAAGTTAAAAACCATC  
ATGTTCTCTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCCTTTTATTAAAGATCCAG  
GTGGAAGATGTTGATGAGCTCTCTCTTTTCTCTTCCATATATGATTATTGAAGTTTGTGA  
AGAAACCCACAGGGATCATTGTAGGCGTGGTGTCTGCCACAGACCAGACAATAGGAAAT  
CTCCTATCAGGTATCTATTACTAGGAGCAAAGTGTTCATATCAATGATAATGGTACAATC  
ACTACAGACTTCTAGTGCATCGTGAATCAGTCTGGTACAACCTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCACTGTATGTGCAAGTTCTTAAACATCA  
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAGTGGATAGAGATGAATCCATAGAAGAGCACCATT  
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAGTTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCAATTTTGACTAATAGAACCTGGTTTAAACCTTCAAGAAGAACCCTGCTTC  
TACATCTCCATCTTAATTGCGCACAATGGAATCCCGTCACTTACAAGTACAACACCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAGACAGAAGTTATCATTTGCTATTCTCATTTGCAATTATGATCATA  
TTTGGGTTTATTTTTTGACTTTGGGTTTAAAAACAACGGAGAAAAACAGATTCTATTTCTGTA  
GAAAAGTGAAGATTTTCAGAGAGAATATATTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATCGGGAACGCAAGACT  
CGGAAACCAACAAGCGCTGAGATCAGGAGCCTATACAGGCGAGTCTTTGCAAGTTGGCCCCGA  
CAGTGCCATATTCAGGAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCCGTGTG  
CCCTCTCTTTGATTCCCTCCAGACCTACGCTTTTGAGGGAACAGGGTCATTTAGTCTGGATCC  
CTGAGCTCTTTAGAATCAGCAGTCTCTGATCAGGATGAAGCTATGATTACCTTTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTCTGCAAGTGAGTCAAAATAATTAGG  
GCTTTTACCATCAAAATTTTAAAAGTGCTAATGTGTTATCGAACCAATGGTAGTCTTAA  
AGAGTTTGTGCGCTGGCTCTATGGCGGGGAAGCCCTAGTCTATGGAGTTTCTGAGTTTCTG  
CTGGAGTAAATACTCCATGGTTATTTTAAAGCTACCTACATGCTGTCTATTGAACAGAGATGTG  
GGGAGAATGTAAACAATCAGCTCACAGGCATCAATACACACAGATTGAAGTAAATAATG  
TAGGAAGATATTTAAAGTAGATGAGAGGACAAGAATGTAGTGCATCTTATGCGGATTTAT  
CATTTATTTACTTAGGAAGAGTAAAAATACCAACAGAGAAAAATTTAAGGAGCAAAAATTTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAATGTATAGTCAGAGAAATTTTCAATGAATTAATCCATGAAGTATTGTTTCTTTAT  
TTAA

0975192.101501

## FIGURE 95

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906  
><subunit 1 of 1, 772 aa, 1 stop  
><MW: 87002, pI: 4.64, NX(S/T): 8  
MNCYLLLRFMLGIPLLWPCLGATENSQTKVKVQPVRSHLRVKRGWVWNQFFVPEEMNTTSHH  
IGQLRSDLDNGNNSFYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVSDDINDNEPKFLDEPYEAIVPEMSPGTLVIQVTASDADDPSSGNNARL  
LYSLLQGQPYFSVEPTTGVRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLSD  
VNDNKPIFKESLYRLTVSESAPTGTSGITIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TQEGIVILKKKVDFEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYVVFVEFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR  
DESEBHHFYFNLSVEDTNSSFTIIDNQDNTAVILTNRTGPNLQEEFVFIISILIADNGIP  
SLTSTNLTIIHVDCDGSSTQTCQYQELVLSMGFKTEVIIAILICIMIIIFGFIFLTLGLKQ  
RRKQILFPKESDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMREKRKRTTSAEIRSLY  
RQSLQVGPDSAIFRKFILEKLEBANTDFCAPPFDSLQTYAFEGTGLAGSLSSLESASVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 597-617

#### **N-glycosylation sites.**

amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537

#### **Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254



## FIGURE 96

ATTTCAAGGCCAGCCATATTTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTGCAACATTGACATTATT

09978492.101501

# FIGURE 97

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCGCCCCGGGCGCGGACCCCAACCCCGAC  
 CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACTTCCTCCGCGGGG  
 CCCAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACTCTCCGCCTTCTGCACCTGCCA  
 CCCCTGAGCCAGCGCGGGCCCCGAGCGAGTCAATGGCCAAACGCGGGGCTGCAGCTGTTGGGC  
 TTCATTCTCGCCTTCTCGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
 GATTACTCCGTATGCCGGCCACAACATCGTGACCGCCAGGCCATGTACGAGGGGCTGTGGA  
 TGTCTCGGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGTGTAAT  
 CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTGGCATCTCTCGGAGTGAT  
 AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGC  
 AGAAGATGAGGATGGCTGTCTATTGGGGGTGCGATATTTCTTCTTGCAGGCTCGGCTATTTTA  
 GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCATGACCCAGT  
 CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTGCCC  
 TTCGGGAGGTGCCCTACTTTGTCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA  
 AGGCCCTATCCAAAACTGCACCTTCCAGCGGGAAGACTACGTGTGAACAGAGGCCAAAG  
 GAGAAATCATGTTGAAACAAACCGAAATGGACATTGAGATACTATCATTAAACATTAGGAC  
 CTTGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAAACAAACAAACAA  
 ACCCATGTGTAAAAAATCTCAGTGTCAAACATGGCTTAATCTTATTTTCTTTCTCTCA  
 ATATAGGAGGGGAAGATTTTTCCATTGTATTACTGCTTCCCATTGAGATAATCATCTCAAT  
 GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATATAGTGTTTTTCTATTA  
 ATAGACAGTAAATACTATTCTCATTATGTTGATACTAGCATACTTAAATATCTCTAAAT  
 AGGTAATGTATTTAATTCATATATGATGAAGATGTTTATGGTATATTTCTTTTTCGTCC  
 TTAATACATATGTAACAGTCAAATATCATTACTCTTCTTCAATAGCTTTGGGTGCCCTTG  
 CCACAAGCCTAGCCTAAATTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTT  
 CATATACTTATTTTATTTTTTACCATAATCTTATAGCACTTGCATTGTTATTAAGCCCTAT  
 TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTTA  
 GTTTCTAAAGCCAAGAAGAAATTTATTACAAATCAGAACTTTGGAGGCCAAATCTTTCTGCATG  
 ACCAAAGTGATAAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT  
 CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT  
 AACACAACCTTTATGATTGAATTTTAAAGCTACTTATTCATAGTTTTATATCCCCCTAACT  
 ACCTTTTTGTTCCTCATTCCTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTTA  
 TATCTTCTTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
 ATCTGGTGACAAATATTTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT  
 TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTA  
 TTAGTTTATATTACTCTTATTTCTTGAACATGAACATATGCCTATGTAGTGCTTTTATTGTCT  
 CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAACCTACACACGTACCTTCATGTGATT  
 CACTGCCCTTCTCTCTACAGTCTATTTCCACTGAACAAACCTACACATACCTTCTCAT  
 GTGGTTCAGTGCCCTTCTCTCTTACCAGTCTATTTCCTGAAACAAACCTACGCAATAC  
 CTCTATGGTCTCAGTGCCCTTCTCTCTTACCAGTCTATTTCCTATTTCTCAGCTGTGCT  
 GACATGTTTGTGCTCTGTTCCATTTAACAACATGCTCTTACTTTTCCAGTCTGTACAGAATG  
 CTATTTCACTTGACAGAGATGTGAATGGAAGGGTGTGGCATCTGTGCTCGGAGCCTG  
 GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTGGCTGCTGTAA  
 GCTTATGCTCTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCACCTCACAGTGATG  
 TTGTTGGGATCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAGTGCTAT  
 ACTAAGGGAAAGAAATTGAGGAATTAAGTCATACGTTTTGGTGTGCTTTTCAAATGTTTGA  
 AAATAAAAAAATGTTAAG

0973132.101501

## **FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185  
><subunit 1 of 1, 211 aa, 1 stop  
><MW: 22744, pI: 8.51, NX(S/T): 1  
MANAGLQLLGFI LAF LGWIGAIVSTALPQWRIYSYAGDNIVTAQAMY EGLWMSCV SQSTGQI  
QCKVFD SLLNLSSTLQATRALMVVG ILLGVIAIFVATVGMKCMKCLEDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMTFVNARYEFGQALFTGWAAASLCLLGALLCCSC  
PRKTTSYPTPRPYPKPAPSSGKDYV

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

#### **N-glycosylation site.**

amino acids 72-75

#### **PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

#### **ABC-2 type transport system integral membrane protein**

amino acids 119-133

03975432.401504

## FIGURE 99

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTGCGAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGGC  
GCGATATTTCTTCTTGACGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCGCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCTGTCCC

09978192.101501

## FIGURE 100

ACCCTTGACCCAACGCGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCCTTCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTCGAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTTCATTGGGGGCGCGATATTTCTTCTTGCAAGTCTGGCTA  
TTTLAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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## FIGURE 101

GGGCCCAGACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTCGCAGANCAACGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNCGAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATTGGGGCGCGATATTTCTT  
CTTGACAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCCTATGACCCCACTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCTGCGA

0970192.101501

## FIGURE 102

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTACCGAGGGGCTTTGGATGTCNT  
GCNTGTGCGAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGC'TTGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCAATTGGGGGCGCGATATTTCTGTGTCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNNTTCNNGNNNTCTATGACCCCTATGACCCCAGTCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTCTCTGTCCC

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## **FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCCTTGAAGGTGGTTGNCATCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGGATATTTCTTCTTGCAAGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCCTATGACCCCAAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCTCTGTCCCGAA

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## FIGURE 104

AGCAATGCCCTGCCCCAGTGGAGGATTAATTCCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTGCGAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGAATGAAGTGTATGA  
AGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCAATGGGGGCGCGATATTT  
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAATNGTTCAAGA  
ATTTTATGACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTTCTGCCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTGCGAACC

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## FIGURE 105

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCCTATGACCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTCTTG

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## FIGURE 106

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCAATTGGGGGCGCGATATTTCTTCTTGCGAGGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCACG

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## FIGURE 107

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNTGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCCTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTTGCTGTTCTCTGCGAA

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# FIGURE 108

GCCTGCCGTCAGCTCGCCGGGCACCGCGGCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC  
 CGCGTAGACCGACCCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCGCCCGTGCCTCCG  
 ACCGCTCCCCGCTTTTGTAAAACTTAAAGCGGGCGCAGCATTAACGCTTCCCGCCCCGGT  
 GACCTCTCAGGGGTCTCCCGCCAAAGGTGCTCCGCGCTAAGGAACATGCGGAAGGTGGAG  
 CAGGTCCTGAGCCTCGAGCCGACGACGAGCTCAAATCCGAGGTCCCTTACCCGATGTTGT  
 CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA  
 CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATCAGGGGCTCAATT  
 AATGTATCTGTGATGTTACAGCCTTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
 TATGGTTCAGTCTATGTTTGTCTCAACTGACACTTCAGATATGGAAGCAGATGGAAGGAGG  
 CAAAACCGGAAGACCTTTATGGATTCAAACCTTAGATGTGTGTTGAATTGCCAGCAGAGAAT  
 GATAAACACATGATGTAGAAATAAATAAAATATATCCACAACCTGCATCAAAGACAGAAAC  
 ACCAATAGTGTCTAAGTCTCTGAGTTCCTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
 AAGAATGTAAGAGGCTCAAGGTGAAGTTGAGAGGCTACGGGAGGAGAACAGCAGTTCAAG  
 GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCATTTTCAGCATTAGC  
 CCAACTGGGAAGGAAGAAGGCCCTTAGCACCCGGCTCTTGCTCTGTTGGTCTTTGTTCTTTA  
 TCGTTGGTGTAATTATTGGGAAGATTGCTTTGTAGAGGTAGCATGCACAGGATGGTAAATTG  
 GATTGGTGGATCCACCATATCATGGGATTTAAATTTTATCATAAACCATGTGTAAGAAAGAAAT  
 AATGTATGATGACATCTCACAGGTCTTGCTTTAAATTACCCCTCCCTGCACACACATACAC  
 AGATACACACACAAATATAATGTAAACGATCTTTTGAAGGTTAAATATGTATGTAAGT  
 ATTGAGGGGGAAAAAGAAATGATCTTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
 GGCATATTGTAATGTCAATTTAAACATTGGTAGGCCCTTGGTACATGATGCTGGATTACCTC  
 TCTTAAATGACACCTTCCCTCGCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCAGCAT  
 GCTGGGGAGTGGGTGAGCTCCACACAGTAGTCCCAAGTGGGCCACTCCCGCCAGGCTG  
 CTTTCCGTGCTCTCAGTTCGTCTCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCA  
 AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
 TGACTGATTGACCCAGCGCTTTGGAATAAATGGCAGTGCTTTGTTCACCTAAAGGGACCAA  
 GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTATTTCAGAGATGTTTAAATGCATA  
 TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTACAAAGAGTACAGTTAATGC  
 TCGCTGCTGCTGAACCTCTGTTGGGTGAACGTGTTATGCTGCTGGAGGGCTGTGGGCTCCTCT  
 GTCTCTGGAGAGTCTGGTCAATGTGGAGGTGGGGTTTTATTGGGATGCTGGAGAAGAGCTGCCA  
 GGAAGTGTTTTTCTGGGTGAGTAAATAACAACGTGTCATAGGGAGGGAAATCTCAGTAGTG  
 ACAGTCAACTCTAGGTTACCTTTTTTAATGAAGAGTAGTCAGTCTCTAGATTGTTCTTATA  
 CCACCTCTCAACCATTACTCACACTTCCAGCGCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
 TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
 ACCAGCAGTTTGGGTGGGGAGCAAGGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
 TAGTTGAGAGTTTGAAGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTCTGTTTGA  
 CTATGTAGCATCTTGAAAGAAAAATATAATAAAGCCCCAAATTAAGAAAA

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## FIGURE 109

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVL~~S~~LEPQHELKFRGPF~~T~~DVVTTNLKLG~~N~~PTDRNVC~~F~~KVKT~~T~~APRRYCVRPN~~S~~GIID  
AGASIN~~V~~SVMLQ~~P~~FDYDPNEKSKHKFMVQSMFAP~~T~~DTSDMEAVWKEAKPEDLMDSKLR~~C~~VFE  
LPAENDKPHDVEINKIIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLRM~~R~~KTVQSN~~S~~PISALAPT~~G~~KEEGLSTRLLALVVLFFIVGVII~~G~~KIAL

### **Important features:**

#### **Transmembrane domain:**

amino acids 224-239

#### **N-glycosylation site.**

amino acids 68-71

#### **N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

09973192 401504  
105107 26127660

## FIGURE 110

GTCA GTCTTCTAGATTGT CCTTATCC CACCTTTCA ACCANTACTCACATTTCNAGCGCCAG  
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGNNAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTGTCAATTTGTCAATTTGCTCTATGGGGGAATTATTATTTT  
ATCATTTTATTATTTTGCATTGGAAGGTTAACTTTAAAATGAGC

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## FIGURE 111

TATTGTAAAGGCCATTTTAAACCATTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNNTTCCTCGCCTGTTGGTGCTGGCCNNTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCAGGCTGCTTT  
CCGTGTCCTTCAGTTCGTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATGTGCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACCTCTGTTGGGTGAACCTGGTATTGCTGCTGGAGGGCTG

05573392.101504



## FIGURE 112

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNCGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAAAGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

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# FIGURE 113

GGTGGCCCATTCCTGGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTTANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGT  
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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## FIGURE 114

TGCTTTCCGTGTCCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTA CT CGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAC TGTTATTCAGAGATGTTTAATGC  
ATATTAACTTATTTAATGTATTT CATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

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## FIGURE 115

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACNTGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCANTCCC  
GGCCCAGGCTGCTTCCGTGCTTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTTGTANIGATTGACCCAGCGCTTTGGAAATAAAATGGCAGTGCTTTGTTTCANTT  
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTTCAGAGATG  
TTTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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## FIGURE 116

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCCAGGCTGCTTCCGTGTCTTCAGTTCGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTGGAAATAAATGGC  
AGTGCTTTGTTCACCTTAAAGGGACCAAGCTAAATTGTATTGGTTCATGTAGTGAAGTCAAA  
CTGTTATTCAGAGATGTTTAAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTC  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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# FIGURE 117

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
 GGCTCCCAGCTGCAGCGTCCCCGCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
 CTCGGGGACCAACAAAGCTTGGCAGGGTCTCACTTTGTGGCCAGGCTGGAGTTTCAGTGCCA  
 TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAAGCGATCCTGCTGAGTAGCTGGGA  
 CTACAGGACAAAAATTAGAGATCAAAATGGAAAAATATGCTGCTTTGGTTGATATTTTCCACC  
 CCTGGGTGGACCCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
 GGTACCCCGGATTTGCAGTGAAAGGACTTTCCATCTCACCAGCCCCGCAATTGAGGCGAGATG  
 CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCACTCCAGC  
 CTTTCTGAAATGGAGGATTATCTTTCCATGAGACTGTCTTTGAGAAATGGCACCAGAACCTT  
 AACCCAGGTTGAAAGTTCAAGATTGGTTCTTGAGCCGACTCAAAATATCACCACAAAGGGAG  
 TATCTGTTAGGAGAAAGACAGGTTGATGGCACCAGCAGGTTTACGATCTTGAGCAAAA  
 AGGTTCTTAACCAATTTCCCTTTTCAACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
 TCTCATTTCCCTCAGCATGTTCTAATGCTGCCCACTGTGTTTCATGATGGAAAGGACTATG  
 TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
 AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC  
 CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAGAAGAAAAAAATCTGGCCGGGCTC  
 AGAGGATTGCCGAAGGGAGGCCCTTCCTTTTCAGTGGACCCGGGTCAAGAATACCCACATTCGG  
 AAGGGCTGGGCACAGGAGGCGATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA  
 GCTGAAGCTGTCTCACAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA  
 TGCCTGGTGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT  
 CGGTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTTACCAATACTGCGATGCTGAGTC  
 GGGCTCCACCGGTTCCGGGGTCTATCTGCGCTCGAAAGATCCAGACAAAAGAAATTTGAAGC  
 GCAAAATCATTGCGGTTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGAC  
 TACAACGTTGCTGTTTCGCATCACTCCCTAAAAATACGCCCAGATTTGCTCTGGATTTCACGG  
 GAACGATGCCAATTTGTGCTTACGGCTTAAACAGAGACTGAAACAGGGGGGTGATCATCTAAA  
 TCACAGAGAAAAACAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
 GAACCTCTGTCAATAGCATTTCACATTTTCAAATCAGGAGATTTTCGCTCCATTTAAAAAA  
 TGTATAGGTGCAGATATTGAAACTAGGTGGGCACTTCAATGCCAAGTATATACTCTTCTTTA  
 CATGGTGTAGTATTTTATTTGTAGAAAAATTTTGTTCGCTTCTTAAAAATTAGACACACTTT  
 AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTTCTCAGGGTCC  
 TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAATGTGAAATTGCATAGATAAAA  
 GGTAGATGGTAAAGCAATTAGTATCAGATCAGACAGAAAGTTTACAACACAGTTTGTACTA  
 CTCTGAGATGGATCCATTTCAGCTCATGCCCTCAATGTTTATATTGTGTATCTGTTGGGCTCT  
 GGGACATTTAGTTTATTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATATAAA  
 CAAACTAATACTGTTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAAA  
 TGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTGAATAAGGGAAGCTGAGACATTT  
 TAAGATCTCAAGTTTTTATTTAACTAATACTCAAAATATGGACTTTTCATGTATGCATAGGG  
 AAGACATTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTTTATGCTATACAT  
 TCTATGTATGAGGTGCTACATTTTGGACAAAGAATTCGTAAATCTTTTCAAGAAAGAGT  
 CTTTTCTCCTTGCACAAATCCAGCTTTTGTATGAGGACTATAGGTTGAATCTCTGATTAG  
 TAATTTTATAGATATGCTCCTTTCCCTAAAAATGAATAAAATTTATGAATATGA

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## FIGURE 118

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAPEADAKMMVNTVC  
GIECQKBLPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTGVSVRKRQV  
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISQHVLTAAHCVHDGKDYVKGSKKLRV  
GLLKMRNKS GGKRRGSKRSRREASGGDQREGTREHLQERAKGRRRRKKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCSVSDESNDLLYQYCDAESGSTSGVYLRLKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

**Important features:**

**Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

**Glycosaminoglycan attachment site.**

amino acids 236-239

**Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

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## FIGURE 119

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCACTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGCAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTT  
CTGCTCCTGAGTTCCAGGACCCGACGCTCCGAGGAGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCCGGGGAGGGGCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCACCAGAAAGCAGGTGATTTCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCTGTGTCTAATGACCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCCCTGGTTGTTGAACCTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGCTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCAGCTCTCCGCAACCAATCCGATGATACT  
GTGGTTGCACTTCCCTATGGAAGTAGACATATTGCGCTTGTCTTAAAGGTCTGATCACTT  
ATATCTGGAACCAAAACCCCTCCAGGGGACTAAAGGTGAAAACAGCTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTGCTAACTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCTTCCCTCGGTGGGAGGCCACCCATGGACCGGTGCTCCTCC  
TCGTGTGGGGGGGCATCCAGAGCCGGGCAGTTTCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTCAGTGGAAGAGTGGAAATGCATGTACACCCCTAAGATGCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCTCTGCACTCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCAAAAACAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTGTCAGAGGAGCCCTCGTAAAGTTGTAAAAGCACAGACTGTTCTATA  
TTTGAAACTGTTTGTGTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAGATTGATTAGTTTCAA  
AAAAAAAA

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## FIGURE 120

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLFLAFLLLSSRTARSEEDRDGLWDAGPWSECSRTC GGASYS LRRLCLS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCSLKCQ  
AKGTTLVVELAPKVLDTGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLVLGKPDHLYLETKTLQGTGKGENSLSSSTGTFL  
VDNSSVDFQKFDPKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRBTDFPFCS  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTCGQGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKLPEAKLPWFKQAQELEEGA AVSEEPS

**Important features:**

**Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

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## FIGURE 121

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCCGGTGGGCCCTCGGGCCTGAC  
AGATGGCAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGCGCTGTGGCTGGCG  
GCCCGCCGGTTCGTGGGGCCAGGGTCCAGCGGCTGCGCAGAGGGCGGGACCCCGGCCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGCGAAACAGCGGCCTGGGCCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTACCAATCTTCTCCTTGGACTCCTCAAAGTTCAGCTCCAGCA  
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACTGGCTAACATTCTTTT  
TACCAGGGAAGTACCCCGCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTGTCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTCAAAACCTCCAGTAGAAGGTGCCAGACTTCCATTTATTT  
GGCCTCTTACCTGAGGTAGAAGGAGTGTGAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAAAGGAACAAGGAGTAAAGAGCTGTTTATAAAAACCTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTGTACTTTGAAGAAAAAGAAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATATATTTT  
TGGGATAAGAGAATTTGAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATACAATTATATTGTAATAATAACTGGGCAAGCATGGATGACATATTA  
ATATTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAATATCTCG  
CTGGTGTGTGCACACAAGTCTTACTTGAATAAAATTTACTGGTAC

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## FIGURE 122

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRRELQAACGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNHIGHFLLTNLLLGLLKSSAPSR  
IVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGNTNVTNVNLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

### **Important features:**

#### **Signal peptide:**

amino acids 1-21

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

#### **N-glycosylation site.**

amino acids 212-215 and 239-242

09978192-101501

## FIGURE 123

GGGGATTGTAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTGGGATAAGAGAATTTGAGCAAAGATGTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA  
AGCATGGATGACATATTAATATTTGTGAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

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# FIGURE 124

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCCGCTCCCGAGCCCAGCC  
 CTTTCCTAACCCCAACCCAACTAGCCAGTCCCAGCCGCCAGCGCTGTCCCTGTCACGGAC  
 CCCAGCGTTACCATGATCCTGCGCTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
 GCTCCTGGTAACCTTGGGTTTTACTCCTGTAACAACTGAAATAACAAGTCTTGCTACAGAGA  
 ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT  
 CGTTTCAGTCAGATGTTGCATCCAATTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
 TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGCATAGCCC  
 AGAGATACAGGATAAGCAAATACCCAACCTCAAATGTTTTCGTAATGGGATGATGATGAAG  
 AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAG  
 TGACCCCAATTCAAGAAATTCGGGACTTAGCAGAAATCACCCTCTTGATCGCAGCAAAAGAA  
 ATATCATTTGGATATTTTTGAGCAAAAGGACTCGGACAACATATAGAGTTTTTGAACGAGTAGCG  
 AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTTCAAAACCGGAAAG  
 ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGATATGGTGTACT  
 TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTTT  
 GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
 ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCAGAATGAAGTAGCTCGGC  
 AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
 CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCTCTGTAATCGCTATTGACAGCTTTAG  
 GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCAAGCAATTG  
 TATTTGACTTACATTTCTGGAAAACGCACAGAGAATTCATCATGGACCTGACCCAACTGAT  
 ACAGCCCAGGAGAGCAAGCCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
 ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAAACCTG  
 AAAAAACAGTTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAATAGTAAACCTA  
 TATTTTCATAATTCATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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## FIGURE 125

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTETISLATENIDEILNNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVFARVDCDQHSDDIAQRYRISKYPTLKLFRNGMMMKREYR  
GQRSVKALADYIRQKSDPIQEIIRDLAETITLDRSKRNIIGYFEQKDSDNVRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFVDVTYNWIQDKCVPLVREI  
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFHRMYVFGDFKDVLIIPGKLQFVFDLHSGKLRHREFHHGPDPTDTAPG  
EQAQDVASSPPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:**

**Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

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## FIGURE 126

ATTAAGGAAGAATTTCCAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCAGAGATACAGGATAAGCAAATACCCAACCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

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## FIGURE 127

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNNGGAGCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCGCTGGAGAATCCTCCGCTGCCGTGGCTCCCGGAGCCCAGCCCTTTCCTAACCC  
AACCACCTAGCCCGTCCAGCCGCCAGCGCCTGTCCCTGTNCGGANCCAGCGTNACC  
ATGCATCCTGCCGTCTTCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTATGCTGACTGGTGTCGTTTCAGTCAG  
ATGTGGCATCCAATTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTGTCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

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## FIGURE 128

GCCCACGCGTCCGATGGCGTTACAGTTCGCGGCCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTGTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCTGAATCCCCCTTGACTCCCAGAGTACCTCAT  
CCACGCTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCTACAACCATCATGAATGCAGATATTCTAGCATATTGTGAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTGCTTGTGGAAAGACTG  
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTTGACAGGTTTGAACCTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTACTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACCTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAAACTTCATGGGTTTCCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTACAAAAATAAAAAGCGGGAATTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTCAGG  
TACTACAGATTTTCAAACCTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCTTTAGT  
GCAATACAATAAAACTCTGAAATTAAGACTC

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## FIGURE 129

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Type II transmembrane domain:**

amino acids 11-31

#### **Other transmembrane domain:**

amino acids 57-77 and 123-143

09978192.101501

# FIGURE 130

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCCTG  
AATCCCCTTGTA CTCCAGAGTACCTCATCCACGCTTTCTTCTGTGT CATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCCTCTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTATCTTCTAGCATTTT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAAACACAGAAGAATT  
GGTCCAGTTAAGTG CATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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## FIGURE 131

CGGACGCGTGGGGGAAACCTTCCGAGAAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAAACAAGATGCGCGGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGCGGGACCGCTTCGGCTGAAGCATTGTAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCACTTGACCTACCCCTTGACAC  
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTGTCT  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC  
ATTCGCTGAACTGAGACAAGAACAACTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCACTTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTATCTTCAAGCGATGACGGAAAAATAGTTATATTCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAAATGAGAAATTCACAAGCGCACAGGAATTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTAAAGATGCCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT  
TGTCCTCTCGGTGATGGTATTGCTTTGGATTGTGTGCAACTGTGTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTTGTGGTTGTTAGATCTAAAACCTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGAATAGACATCTAAAATTCACCTCCTCATAGAGCTTTTAAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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## FIGURE 132

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGS LWVRTQLGLPPLLLLT MALAGSGTASAEAFDSVLGDTASCHRAQLTYPLHTYP  
KEEELYACQRGCR LFSICQFVDDGIDLNR TKLECESACTEAYSQSDEQYACHLGCONQLPFA  
ELRQEQLMSLMPKMHL LFP LTLVRSFWSDMMDSAQSFITSSWTFYLQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSY LQMRNSQAHRNFLEDGESDGF LRCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDL EFMNEQKLNRYPASSLVVVRSKTEDHHEAG  
PLPTKVNLAHSEI

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 241-260

#### **N-glycosylation site.**

amino acids 90-93

00070132.101501

# FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATTCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTGCG  
TGAAGTGAACAAGAACAATTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

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## FIGURE 134

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAAC TGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTGGGGGACCG  
CTTCGGCTGAAGCATTTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCTAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

0978192-101501

# FIGURE 135

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCGGAGGT  
 GGGGCGCCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCGCGACCGAGC  
 GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGCCGCGGCTG  
 GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
 AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT  
 ACCTGTGATGTTGAAACCATTGATAGATTTAATACTACAGGCTTTTCCCAAGACTACAAA  
 ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT  
 GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
 GTTCTGTATGGAATTAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATATCTCATTGA  
 AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
 AGGCTGTTCTTCAGTGGACCAAGCATGATGATTTCTTCAGATAAATTCTGTGAAGCTGATGAC  
 ATTCAGTCCCCGTAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
 CAAGGGACCAGATGCTTGGAAAAATATGGAATGTCTACGAAGAAAACTGTTTAAAGCCAC  
 AGACAATTAAGACCTTTAAATCCTTTGGCTTCTGTGTAAGGACAACTGAAGAGAACACT  
 TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTTCTACAGACTTATATCTGG  
 CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAGAGACCTGGTTAG  
 AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGACTGAA  
 GGAGAAGGTCCAAGAAGGCTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
 ATCCAAAGTGTTACCAATTCTTCGAGCGCCAGATTTTCAACTCTTTACTGAAATAAAATTC  
 AGGATGAGGAAAACAAATGTACTTCTGGAATACTTCATGAAATCAAGTCATTTCTTTG  
 CATTTTGATGAGAATTCATTTTTTGTCTGGGGATAAAAAAGAAGCACAACTAAAGGAGGA  
 CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
 GTCTGTGGGGAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
 AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCATCTAACCAGACAAGA  
 AATAGTATCATTTATCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAT  
 TCAGGAACCTGTTACAGAATATTCATTAAAGAAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
 AATGGAGGCGAAGAGTGAATTTTCAATCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
 ACATTTTATATAAAGTTGCTTTTGTAAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT  
 AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG  
 GTACAAATTTTAAAGTTTAAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

09978192.101501



## **FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974  
<subunit 1 of 1, 468 aa, 1 stop  
<MW: 54393, pI: 5.63, NX(S/T): 2  
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAQRCFCQVSGYLDCTCDVETIDRFNNYRLF  
PRLQKLLESDYFRYYKVNLRPCPFWNDISQCGRDCAVKPCQSDEVPDGIKSASYKYSEEA  
NNLIEECQAERLGAVDESLSSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAYVDLLLNPE  
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRLASKVLPFFERPDPQLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTQGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **N-glycosylation site.**

amino acids 280-283 and 384-387

#### **Amidation site.**

amino acids 94-97

#### **Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

#### **Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

#### **Interleukin-7 proteins**

amino acids 338-343

09978192-101501

## FIGURE 137

GCTGGAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGAAGGAGAAGGTC CAAGAAGG  
CTTAAGAAC TTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT  
CTTNGAGCGCCAGATTTTCAACTNNTTTACTGGAATAAAATT CAGGATGAGGNAAACAAA  
TGTTACTTTTGAAAATACTTCATGAAATCAAGTCATTTCTTTGCATTTTGATGAGAATTCA  
TTTTTTTGCTG

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## FIGURE 138

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATCTGGACAGAAAC  
CGATCAGGCATGGAACTCCCCCTTCGCTACTCACCTGTTCTTGGCCCTGGTGTTCCTGCACAGG  
TCTCTGCTCCCCCTTTAACTGGATGAACATCACCCACGCCTATTCCACAGGGCCACCAGAAG  
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCCTTCAGGCGACCGGAGGGGGACGCTTTATCGCTGCCCTGTAGGGGG  
GGCCCAATGCCCATGTGCCAAGGGCCACTTAGGTGACTACCACTGGGAAATTCTATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTCT  
ATGGTGAGCTAAAGGAGAGGGGTGGTGGCAGTGTCTCTGAAGGTCATATAAAGAAAAAAGAGAA  
GTGTGGTAAGGGAAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAAACCTAGAAAGCAAA  
AGGTAGGTAATGTACAGGGAGTAGTCTTCATGCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAATATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCAACGTGAGCCAGAGGAAGCCTGAGTACTTGGTT  
CCCAGAAGGAGATACCTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATGTGCTACCTAATGTGCTTGCAAAGCTCCATGTTTCTTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTCAAGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT  
CTCTACTAAAAAATAACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTC  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAA  
AATAATAATAATAATAATTAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTTAAAAAT

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## FIGURE 139

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039

><subunit 1 of 1, 124 aa, 1 stop

><MW: 13352, pI: 5.99, NX(S/T): 1

MELPFVTHLFLPLVFLTGLCSFPNLDEHHPRLFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW  
DGPSGDRRGDVYRCFVGGAHNAPCAKGLGDYQLGNSSHPAVNMHLGMSLLETDDGGGMVS

**Important features:**

**Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 70-73

**N-glycosylation site.**

amino acids 98-101

**Integrins alpha chain proteins**

amino acids 67-81

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## FIGURE 140

CACAGTTCCCCACCATCACTCCTCCCATTCCTTCCAACCTTTATTTTTAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAACCTCCCTTCGTCACTCACCTGTTCTTG  
CCCCTGGTGTTCCTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGGCCACAATGCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAACTGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGA  
CAGATGGTGATGG

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# FIGURE 141

AAAGTTACATTTTCTCTGGAACTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
 GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTCTGGGCCGGCTCTAGAACA  
 ATTCAGGCTTCTGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
 GAGATGGACAGAAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACTGAGTCTACCA  
 AATGCAGACTTTACAAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
 ACGCATTTGATTCCATGTTTGTCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCCTC  
 TCTGTACTCTCAACCAATGAAGCATCTCTTGATGTGGAGCCCGAGTGATCGCGCTGGAGA  
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
 GGATCCCCCAGCAGCTGGTGTCTCACTCACTGAAGGTCTCTGAGTGTGATGTCACTGATGACATC  
 ACGGCCACTGTGCATACAACCTTCGTGTGAGGGCCACATTGGGCTCAGACACCTCAGCCTG  
 GAGCATCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
 TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCAGAGGAACATGTCAAATGGTGAGGAGTGG  
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGAG  
 CATTCTGTAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
 GGAGAGGCCATTCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT  
 GGTCTGCCACTGTTTCGTCTGGAAAATGGGCGCGCTGCTCCAGTACTCTCTGTTGCCCGTGG  
 TGGTCTCTCCAGACACCTTGAAAAATAACCAATTACCCCCAGAAGTTAATCAGCTGCAGAAGG  
 GAGGAGGTGGATGCTGTGCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCTGGAT  
 CTCATAGGTTTGGCGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC  
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCGCCACCGACAGGGATGAGAGAAGTAGGAAGA  
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTCTGGCTGAGCAACC  
 CTGGGAAAAGTGACTTCATCCCTTCGGTCTTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
 TACACACCTGCTAAACACACACACACAGAGTCTCTCTATATATACACACGTACACATAAA  
 TACACCCAGCACTTGCAAGGCTAGAGGGAACCTGGTGACACTCTACAGTCTGACTGATTGAG  
 TGTCTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
 GGCTTGGAGAGCCCACTTTCCAGAAATAATCCTTGAGAGAAAAGGAATCATGGAGCAATGG  
 TGTTGAGTTCACTTCAAGCCCAATGCCGTTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
 CATGAACCTACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGGAGTGAATGTATGT  
 GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCTCTTTTTC  
 TGTGTGTAAGTACGAATTCAGCAAATAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
 AAAAAAAA

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## FIGURE 142

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLIMWSPVIAPGE  
TVVYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLVRATLGQSQTSAW  
SILKHPFNRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPAAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLVLAFAFVGFMILIV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPPELLRAWIS

### **Important features:**

#### **Signal peptide:**

amino acids 1-29

#### **Transmembrane domain:**

amino acids 230-255

#### **N-glycosylation site.**

amino acids 40-43 and 134-137

#### **Tissue factor proteins.**

amino acids 92-119

#### **Integrins alpha chain proteins**

amino acids 232-262

09978192.101501

## FIGURE 143

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTAATACTTCTGTGCAATACCAGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGCGAACCCCTTGCGGCGCAAGGG  
GTTTNGCGAACCCCTTGCGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTGAGTGGCGCTGGGTTGAT

09078192-101501



## FIGURE 144

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGGGGAACTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCTT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCTGGGGATGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGGTTCTTTATGACCCCTTCTGCCCCATTAAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACTTGTACAACACCGGCCGACATGTCTCCTTCTGCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCGAGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACTTCAACCAGGAACTCTACGGGAATTTAGCGCTGCCTCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCCATTCTT  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGACCCCGCCTGCTCCGAGACTGTCACTTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCCCACAGGGCACTGAGGGGC  
AACAGGGACCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCAACTACCGCCTGCATGTGGA  
TGGTGTCCCCATGGTTCGCTGAGACTCCCTTCGAGGATTGCACCCGCCGCTCTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

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## **FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLTYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLLLFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE  
TVTWILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 177-199

#### **N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

#### **Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

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# FIGURE 146

GGCGCTGGTCTTCGCGCTACTGGCTGTACGGAGCAGGAGCARGAGSTCGCGCCAGCCTCCGCCGCGAGCCCTC  
 GTTCGTGTCCCCGCCCTTCGCTCCTGCAGCTACTGCTCAGAAACGCTTGGGGCGCCACCTGGCAGCTAACGAA  
 CGAGCTCCCTTCCCAACGAGCTGAGGTTCTAATTTTGGAGCGTTTGGCTGCCATTTCTCCAGGTGTGGGAGC  
 CGCAGAGCGGAGGCTCGCGTATTTCTGCAGTTCAGCACCAAGTTCGCCCGCCGGAGCGCTCGGTGCTCAGGCCCTTC  
 CGCAGCGGGGCTCTCCGCTTCGCGGTCCCTTGTGAAGGCTCTGGCGGCTGCAGAGGCGCGGCGCTCCGTTTGGCT  
 CACCTCTCCAGGAACTTCACTCTGGAGAGCCAAAGGAGTGGAGAGCGCTGCTTGGAGATTTTCTCGGGGAA  
 ATCTCGAGGTCACTTATTGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAAACACAGTGTGTTTTCATGGCTAGA  
 GCAATTCAGGCATGGTGGTTCCCAATGCCACTTTATTGGAGAAACTTTTGGAAATAATCATGGATGAGGATGGT  
 GAGTGGTGGATAGCCAAACAGAGGGGAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT  
 AATAAATTCAGAACTCAGGTGTATTCACACGCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA  
 TCTGCAGAACTCTGGCTGGTGAATGTCTGTGGGAACATGGACCTGCAAGCTTGCTCCATCAATGGACAGAAAT  
 TTGGGAGCACACTGGGGAGATATAGGCCCGCCAGCGTTTCATGTACAACCTGTTGGTATGTAGTGAAGTGAAGACTTT  
 AGCTACCCATATGAACATGAATGCACCCATATTGTCCATTCAGGTGTCTGGCCCTGTATGTACACATTATACA  
 CAGGTCTGTGGGCAACTAGTAACAGAACTCGTTTGTGCCATTAATTTTGTGCATAACATGAACATCTGGGGGCGAG  
 ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTAATCTCCCAAAGGGAAACTGGTGGGGCCATGCCCTTACAA  
 CTAGGCGCGCCCTGTTCTGCTTCGCCCACTAGTTTGGAGGGGGCTGTAGAGAAATCTGTGCTACAAAGAAAGG  
 TCAGACAGTATTATCCCCCTCGAGAAGAGGAAACAAATGAATAAGAACGACAGCAGTCAACAGTCCATGACACC  
 CATGTCCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAGCGCACAGCAATGTCCCAAATTTGTTCT  
 TGTGAAGTAAAGATTAAAGATCACTGTCAAGGAACAACCTGCAATAGGTACGAAATGCTCTGGCTGTTTGGAT  
 AGTAAGCTAAAGTTATTGGCAGTGTACATTATGAATGCAATCCAGCATCTGTAGAGTGTCAATTCATTATGGT  
 ATAATAGCAATGATGGTGGTGGGTAGATATCACTAGACAAGGAGAAAGCATATTTCATCAAGTCCAATAGA  
 AATGGTATTCAAACATTTGGCAAATCTGCTCTCAATTCCTCAGACTCTCAAAGTACAGTTTCAGGCTGTGCT  
 ACTTGTGAACCAACTGTGGAACAGCTCTGTCCATTTCAAAAGCTGCTTCAATGTGCCAAGAGTATGATCTGCT  
 CGTAACCTGTATGCAAGCAAAATCCACATTATGCTCTGTGTAATGGAACTCGAGTTTATTTCTGATCTGCTCAGTATC  
 TGCAGAGCAGCAGTACATGCTGGAGTGGTTTCAAAATCAGCGTGGTGTATGTGATGTAATGCTGTGGACGAAAGA  
 AAGACTACATTGCTTCTTTTCAAGATGGAATCTTCTCAGAAAGTTTACAGAACTCTCCAGGAGGAAAGGCATT  
 AGAGTGTGTGCTGTGTGTGAAGTCAATTAATCTGGAAGAGGACCATAAAGACTTCCAAATGCAATATTCTGA  
 ATTTTGTATAAACTGTAACTATCTGTACAGAGTACATCAACTATTTTTCAGCCCAAAAAGGTGCCAATGCTATA  
 TAAATCTTGATAAAACAAAGTCTATAAAATAAAACATGGGACATTAGCTTTGGGAAAAATGAATGAAATATATAGG  
 TTTTGAAGATCCTGTGTAAATATTGCTATATTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCAAGATT  
 GTTCTACGTTTCAATATTATATGGTGTGTTATATGCCCACTAATAAATGAATCTAAACATGAATGTGAATG  
 GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAAACGAAAGAAACCTTATCACTTTTCCCC  
 AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTT  
 TGTAAATTTAGGCATATAGAATAATTAATTTCTGATATTGCACTTTATTTTATATAAAATTAATCCTTTAATATC  
 CAAATGAATCTGTAAAAATGTTTGAATCCTTGGGAATGGCTTAAAAATAAATGTATAAAGTCAGAGTGGTGGT  
 ATGAAAACATTCTAGTGATCATGTAGTAAATGAGGTTAAGCATGGACAGCCAGAGCTTTCTATGTACTGTATA  
 AAATGAGGTCACTATTTTCTTTTGTATCCTGGCAAACTACTCCTGCAGGCGAGGAGTATAATAGCAAAAAGTT  
 GAACAAGATGAACATATGTTATACATTACCATGGCACTGATTTTTTTAAATGTAGTAAATGACCTTTGATATAA  
 ATATTTGCCATATCATGTACTTATAATGGTGAATATTTTCTATGAAAAATGTATTTGCTTTGATACCTAA  
 AATCTGAAAAATGTTAGTTTGGTAAATTTTTTTCTGCTGGTGGATTACATATTAATTTTCTGCTGGTGGGA  
 TAAACATTAAAAATTAATCATGTTTCAAAAAA

09978192.101501

## FIGURE 147

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLEKYMDEDEGEWWIAKQRGKRAITDNDM  
QSILDLHNKLR SQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQV VWATSNRIGCAINLC  
HNMNIWGQIWPKA VYLVCNYS PKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRY  
YPPREEETNEIERQQSQVHDTHVTRSDSSRNEVIS AQQMSQIVSCEVRLRDQCKGTT CNR  
YEC PAGCLDSKAKVIGSVHYEQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGI  
QTIGKYQSANSFTVSKVTQAVTCETTVEQLCPFHKPASHCPRVYCP RNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDMPVDKRKTYIASFQNGIFSESLQNPPGGKAFRV  
FAVV

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

#### **N-glycosylation site**

amino acids 28-31

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## FIGURE 148

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCCGCGCTCCGACGGGCCAGCGCCCTCCCCCATGTCCCTGCTCCACGCCG  
CGCCCCCTCGGTGAGCTGAGGCTCCTGGCGGCCGCGTGCTCCTGTGTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAAGATCCGTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACGTGCGAGGAGAAGATGGTTAT  
CATCACCAACAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCCAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGTTGAAAAACCTCAGAAGGGAAAACTCCAAACCAAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCAGATGGGAGACCCATCTCTTGTGTCT  
CCAGACTTCATCACAGGCTGCTTTTATCAAAAAGGGGAAAACTCATGCCTTTCCTTTTAA  
AAAATGCTTTTGTATTGTCATACGTCACTATACATCTGAGCTTTATAAGCGCCCCGGA  
GGAACAATGAGCTTGGTGGACACATTTATTGCAGTGTTGCTCCATTCTAGCTTTGGGAAGC  
TTCGCTTAGAGGTCTTGGCGCCTCGGCACAGCTGCCACGGGCTCTCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCTGTAGCCGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAAATGTGCTTCATCCCCCCT  
GGTTAATTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGCTTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTACAGCAAAACCTTAGGAGAAAACT  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCCATGTAATCTTCAATGTTAAACAGTGCACTCCTCTTTCGAAAGCTAAGAT  
GACCATGCGCCCTTCTCTGTACATATACCTTAAAGAACGCCCCCTCCACACACTGCCCCC  
CAGTATATGCCGATTTGACTGCTGTGTTATATGCTATGTACATGTGAGAAACATTAGCAT  
TGCATGCAAGTTTCATATTCTTCTAAGATGGAAAGTAATAAAATATATTGTAAATGTAAAA  
AAAAAAAAAA

09370192.101501

## FIGURE 149

MSLLPRRAPPVSMRLAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**Signal sequence:**

amino acids 1-34

09978192.101501

# FIGURE 150

GCCCCAGGGAGTCTGATGGCTTCCTTTGTGTTACCCCGGTCTGCGTCATGTTAAAGTCCAAATGTCCTCCTGTG  
 GTTAACTGCTCTTGCCATCAAGTTTCAACCTCATTGACAGCCAGACAGATATCCAGTTGTCAACACAAATATGG  
 CAAATCCGGGCGCTAAGAACCCGTTACCCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA  
 TGCTCTACCCCCCACTGGAGAGAGCGGTTTACAGCCCCAGAACCCCGTCTCTCTGGAGCTGGCATCCGAAATAC  
 TACTCATGTTTGTCTGTGTGGTCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT  
 TACGCCCAATTTGGATACCTTTGATGACCTATGTTCAAGATCAAATGAAGACTGCCTTTACTTTAAACATCTACGT  
 GCCACCGGAAGATGGAGCCAACACAAAGAAAACGAGATGATATAACCGAGTTAATGACCGTGGTGAAGACGAAGA  
 TATTCTATGATCAGAACAGTAAGAGACCCGTCTATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA  
 CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTCATCGTGATCACCATTAACATACCGTCTGGGAATACT  
 AGGGTTTAAAGTACCGGTGACACAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTCGGGT  
 GATTGAGGAGAATGTGGAGCGCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGCTGGGGCTC  
 CTGTGTACGCTGTTGACCCCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTACAGACGGCACCGC  
 CCTGTCCAGCTGGGCACTGAACTACCAAGCCGGCCAAAGTACACTCGGATATTGGCAGACAGGTGCGCTGCAACAT  
 GCTGGACACCAAGCACTGATGAGTATGCTGCGGAAACAAAGATACAAAGGAGCTCATCAGACAGACCATCACCC  
 GGCCACCTACCAACATAGCCTTTCGGGCGGTGATCGACGGCGACGTCATCCAGACGACCCCCAGATCCTGATGGA  
 CGAAGGCGAGTTCCTCACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCGTGAAGTTCTGGGACGGCAT  
 CGTGGATAACAGGAGCGGTGTGACGCCAACAGACTTTGACTTCTCCGTGTCCAACCTCGTGGAACAACCTTTACGG  
 CTACCTCTGAAGGGAAGACACTTTGCGGGAGACTATCAAGTTTCATGTACACAGACTGGGCGGATAAGGAAAAACCC  
 GGAGACGCGCGGGAAGCCCTGGTGGCTCTCTTTACTGACCACAGTGGGTGGCCCCCGCTGGCGCGCGACCT  
 GCACGCGCAGTACGCTCCCCCACTACTTCTATGCTCTCTATCATCATGTGCAAAAGCGAAATGAAGCCGACCT  
 GGCAGATTTCCGCCCATGTTGATGAGGTCCCTATGCTCTCGGCATCCCCATGATCGGTGCCACCCGAGCTCTTCAG  
 TTGTAATCTTCCAGAAGCAGCTCATGCTCAGCGCGGTGGTTCATGACCTCTGGACGAATTCGCCAAAACCTGG  
 TGATCAAATCAACAGTTTCTCAGGATACCAAGTTTCATTCCACAAAACCTACACCCGCTTTGAAGAAGTGGCGTG  
 GTCCAAAGTATGATCCCAAGACAGCTCTATCTGCATATTGGCTTGAACCCAGAGATGAGAGATCACTACCCGGG  
 AACCAAGTATGCTTCTCTGGAGATCTGTTCTCTCATTTGGCACAACTTGAAGAGATTTCCAGTATTTTCAAC  
 AACCAAAAGGTTCTCCACAGACATGACATCATTTCCCTATGGCACCCCGCGATCTCCCGCAAGATATGGCC  
 AACCAACAAAGCGCCAGCATCACTCTCGCCAAACATCCCAAACTCAAGGACCCCTCAAAACAGGGCGCTCAG  
 GGACACAACTGTCTCTCATTTGAAACCTCAACAGGATATTCCACCGAATTAAGTGTCAACATTCGCTCGGGCGTCTC  
 GTCCTCTTCTCTCAACATCTTAGCTTTTGGCGCTGTGACTACAAAAAGGACAAGAGGCGCATGATGCTCTGCGAT  
 GAAGCAGCTGGAAACAGATCAGAGTGTGAGTCTGCTGACGGCACACGACACACTGAGGCTCACCTGCCCGCCAG  
 CTACACCTCTACGCTGCGCGGTGCGCAGATGACATCCCATTTATGACGCCAAACACCATCACTGATTTCAAA  
 CACACTGACGGGATGCGGCTTTGCACACTTTAACACCTTCAGTGGAGGACAAACAGTACAAATTTACCCCA  
 CGGACATTTCCACCACTAGAGTATAGCTTTGCGCTTATTTCCCTTCTATCTCCTTACCCGTACCCGCTCAGCAACAT  
 AGAAGAGGGAAGGAAGAGAGAAAGGAAGAGAGAGAAAGAAAGTCTCCAGACCGAGGAATGTTTTGTGCCACT  
 GACTTAAGACAAAAATGCAAAAAGGCACTCATCCATCCCGCAGACCCCTTATCGTTGGTGTCTTCCAGTATTAC  
 AAGATCAACTTTTGACCTGTGAAATGTGAGAAGTACACATTTCTGTTAAATAACTGCTTTAAGATCTCTACCA  
 CTCCAATCAATGTTTAGTGTATGAGGACATCACCATTTCAAGGCGCGGTGTTTTCAACGCTGATGGAAGCAGCT  
 GACACTCTGAACTCAGCCAAGGACACTTGATATTTTTTAATTACAAATGGAAGTTAAACATTTCTTTCTGTGC  
 CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTGCCCCAGACATGGAGCTGTAATCCAG  
 AGAGAGGAAACGTAGAAATTTATTTAAAAAGATGGACTGTGACGCGAAATCTGTACCGTTCTGTGCAAGAG  
 GTGTTTTCGACGCTGACTATATTTAAGAGACTTTGT

105101.2618460

## **FIGURE 151**

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVPYASP  
PTGERRFPQPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMLPWFWTANLDTLMTYVQDQN  
EDCLYLNIIYPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTLSHYSEGLFQKAIIQSGTALSSWAVNYQPAKYTRILADKVCNML  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLG  
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYTDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVYV  
FGIPMIGPTELFSCNFSKNDVMLS AVVMTYWTNFAKTGDPNQPV PQDTKFIHTKPNRFEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPDMTS  
FPYGTRRSPAKIWP TTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTE LSVTI AVG  
ASLLFLNILAFAALYYKDKRRHETHRRPSPQRNTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPDYYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

### **Signal sequence:**

amino acids 1-24

### **Transmembrane domains:**

amino acids 189-204, 675-692

09978196-101501



# FIGURE 152

GGGAAAGATGCGCGGCGACTCTGGGACCCCTTGGGTCGTGGCAGCAGTGGCGGCGATGTTTGT  
 CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTTGTTGGGGTCTGGGCAGGGGCCA  
 CAGCAAGTTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTGCGAAGCC  
 CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGTTGA  
 TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCCTTGTGGAACCGG  
 GTGCCATGTTTCTCGAGAGACTGGGAGTTGCAGGTGCACCTTCAAATCCATGGACAAGGAAA  
 GAAGAATCTGCATGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
 CTGTGTTTGGAAAACATGGACAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
 GAGGAGAGCAGCAAGAGCGGGTATTCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT  
 CAGCTATGATCATGAGCGGGATGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
 GCAATCTTCATTACGACACCTTCTGGTGATTCGCTACGTCAAGAGGCATTGACGATAATG  
 ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCGTGC  
 CCGGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
 TTTCTTGAAGTTGTTTGAATGCAGTGGAGAGAACCCAGAAAGGAAAAGCTCCATCGA  
 GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCTGAGATGACAGCTCCACTGCGGCC  
 CTGAGTGGCCCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGTGTTTCTGTATTTGCCA  
 TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
 GCCCTCCTGCTGCCACCACCTTTTGTGACTGTACCCATGAGGTATGGAAGGAGCAGGCACTG  
 GCCTGAGCATGCAAGCCTGGAGAGTGTTCTTGCTCTAGCAGCTGGTTGGGGACTATATTCTG  
 TCACTGGAGTTTGTGAATGCAGGGACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAAT  
 CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCTTTCCCTCGAGTCC  
 TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTACGTGGTTGTGATGCAAAAATCAGAGAAC  
 AGAATTTATAGCCAGGCTGCCGTGTGTTTGACTCAGAAGGCCCTTCTACTTCAGTTTTG  
 AATCCACAAGAAATTAAGAACTGGTAACACCACAGGCTTTCTGACCATCCATTGTTGGGTT  
 TTGCATTTGACCAACCCCTCTGCCTACCTGAGGAGCTTTCTTTGGAACACAGGATGGAACCT  
 TCTTCCCTGCCTTACCTTCTCTTCACTCCATTCAATTGTCTCTCTGTGTGCAACCTGAGCTG  
 GGAAAGGCATTTGGATGCCCTCTCTGTTGGGGCTGGGGCTGCAGAAACACACCTGCGTTTAC  
 TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT  
 GGGTCTTGGGTCTATTGGCATGTCCATGGCCCTTCCAATCAAGTCTCTTCAGGCCCTCAGTG  
 AAGTTTGGCTAAAGGTTGGTGTAAGAAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
 GATTAGCTGTGCAACTGACAGCTCCAGGTTTGATCAAAACCAAAGCAACATTGTGATGTG  
 GTCTGACCATGTGGAGATGTTTCTGGACTGTCTAGAGCCTGCTTAGCTGCATGTTTGTAGT  
 TACGATTTTTGGAATCCACCTTTGAGTGTGTAAGGTGTAAGGAAGCTTCTTCTTACACCTT  
 GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT  
 TGCTGTTCTCATGTTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCGCTGGAAGAGTT  
 CACTGTCAATTGAGCAGCACAGCCTGAGTGTGCGCTCTGTCAACCTTATTCCACTGCCTTA  
 TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAATCAGTTACAGGCCAG  
 AGTCTCCTTGGAGGGCTGGAACCTCTGAGTCTCTTATGAACCTCTGTAGCTTAATGAAAT  
 TCTTAAATCACCAGTGGAAACCAAAAAAAAAAAAAAAAAAGGGCGCCGCGACTCTAGAGTCG  
 ACCTGCAAGTGGGATAACAGGGTAATAAGCTTGGCCGCCATG

09978192.101501

## **FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911  
><subunit 1 of 1, 348 aa, 1 stop  
><MW: 39711, pI: 8.70, NX(S/T): 1  
MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGPGQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKEHGQKKK  
LHGDGLAIWYTKDRMQPGPVFGNMDKFVGLGVFVDITYPNEEKQQERVFPYISAMVNNGSLSY  
DHERDGRPELGGCTAIVRNLYHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKLFEITVERTPEEEKLHRDVFLPSVDNMKLPENTAPLPPLS  
GLALFLIVFFSLVFSVFVFAIVIGIILYNKWQEQSRKRFY

### **Signal sequence:**

amino acids 1-38

### **Transmembrane domain:**

amino acids 310-329

09978192.101501

# FIGURE 154

CCGAGCCGGGCGCGCAGCAGCGAGCTGGGGCCGGCTGGGACCATTGGGCGTGAAGTGCATCTACGGATCAGTCT  
CTGATGGTGGGTGATTAACTCAGTGGGAGCTCCCAAGATTTCATGAAGAAATCAGTTGTCTTCATTCAAGAAAT  
TGGGGTCTGGGCTCAGAAATCTCGCAGCTGGTGAAAAATCTGTTTCTAGAAAGGTTTAAATTAATGCCTGCAGTCT  
GACATGTTCCCGATTAGAGGTGAACCATGAAGAGAAAAAGAAATCTTAATAATGCTTTTCCGCAACCGCTTCT  
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCCTTTGTAGCCCTCAGCCTGCAGTCTTCCACATGATCCCGGTG  
CGACTCTTAAGAATGGAATGAGTAGCAAGAGTTCGAAAGAGAATCATGCCGACCTCTGTGACGGAGCCCCCTGTGA  
CAGACCCGTTTATGAAGCTCTTTGTACTGCAACATCCCACTGGCCAGTGGCGAGCGCAGCATGGAAGGTCATGCCC  
CGCATCATTTAAGCTGGTCTCAGTGCAATGTTTCATTCGCCACGGAGACAGGTACCCACTGTATGTGATTTCCCA  
AAACAAAGCGCACGAAATTTGATGCACTCTGGTGGCTAACAGGAAACCGTATCACCAGAACTGGAAGCTTTCA  
TTAGTCACATGTCAGAAAGGATCCGGAGCTCTTTGAAAGCCCTTGAATCTCTTGCTCTTTACCCAAATCACC  
TCTGTGTGAGATGGGAGAGCTACACAGACAGGAGTTGTGCAGCATTTGACGAACCGTCACTGCTGAGGGATA  
TCTATCTAAAGAAACACAACTCTCTGCCAATGATGGTCTGCAGACAGCTCTATTTAGAGACCACTGGGAAAA  
GCCGACCCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGAAGTGGATGATTTATTTCA  
GGCAGCAGCTCAAGTGGCTGTTCTGCTCTGGAAGCTGCTATTGCCCGGTAAAGAAACAGTATCTGGAAAGGAGC  
AGCGTCTGCTAGTACCTCTCAAGTTTGAAGAACAGCCAGCTGGAGAGACCTACGGGGAGATGGCCAAAGATCGTGG  
ATGTCCTCCACCAAGCAGCTTAGAGCTGCCAACCCCATAGACTCCATGCTCTGCCACTTCTGCCCAATGTCAGCT  
TTCCCTGTACCAAGAAATGGCTGTGTGATGATGGACACTTCAAGGTAATTAAAGACCCATCAGATCGAGGATGAAA  
GGGAAAGACGGGAGAGAAATTTGTAATCTCGGGTATTCTCTCGGGTGGCCACCCCATCTGAAACCAACCATCG  
GCCGATGTCAGCGTGGCCACCGAGGCGAGAAAGAGACTCTTTGCCCTCTACTCTGCTCATGATGTCACTCTGT  
CACCAGCTCTCAGTGCTTTGGGCGCTTTCAGAAAGCAGGTTCCTCAAGTTTTCAGGCGAGGTGATCTTTGAGCTTT  
GGCAGACAGAGAAAGCCCACTGAACTTCCGCTCGGATTCTTTCAATGGCGATGTCACTATTCACACTCCACCT  
CTTTCTGCCAAGACCCACCAAGCGTCTCCCAAGCCCATGTGGCCCTTGAAACTTGGTTCGCTTTGTGAA  
GGGACATGTTTGTAGCCCTGGGTGGCAGTGTACAAATTAATATGATGATGCTACAGAGCATAGGAAAGTCCACTTCTAGTTTGTCTGTAC  
TAAGGTTAGAAGATTATGCTTTTAAAGGCTAAATATGTTTGTGGGAACCAACAGGATTTGGGCTTGAACAT  
AAGCACAATTGCTGCAATGTGGTAGCTGAATGCTTGGTACAAAGTGGCCAGTCTCAGAGAGATAGAAGGTACTT  
TATCATAGCCAGACTTCGCTTAGAATGCCAGAAATATATAGTTCAAGACCTGGAAGTGGCCAACTCAAGTTTGCAC  
TCTTCTGGCCCTGCCCATGTTATGATGATGGAACAGCACAACCTCAACAAAAATTTTAAATCTTAGACATT  
TTTACCTTGTCTTGTGAAGAATTTCTTGAAGTGAATTTATCTAAATAAAGGTTGGCAAACTTTTCTGTGAAGG  
GCCAGATTGTAATATTTTCAGACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCTAACTACTCAACTCTGT  
TTCTGAAGCAGGAAGCCACCAAGACAGTACATAAAGGAATATGTGTAGCTGGGTTCGAGGCCAGACAAACCA  
GATGTTGACAGACTTGGCCCTGGGCTGTAGTTTGTGACCCCTCATCTAAAAAAATAGGCTATATCAATTGC  
ACTTCAGCACTTTGAGAACGAGTTGAATACCAAGAAATTTCAATGGTTCCTCCAGTAACTCTGCTAGAAACA  
CAGAAATTTGGTCTGATCTGACAGTACAGAAACAAACCTGAGGGTAATAAACAATGAATTAAGATGAATCATAGAA  
AACTGATTAGAAGAACTTGTATGTTTATGATGATTTGTGTAACAAGATAGTTTAAAGTATGTTCTAAATATTGT  
CTGCTGTAGTCTATTGTGCTATATGCTGAAATTTTGTATGCCATTAGTATTTTTATAGTTTGAAGAAATATT  
TTCTAAGACCAAGTTTAGATGACTCTTATCTCTGTAGTAATATCAATTTGCTGTACCTGCTGGTGGTTAGAAG  
GAGGCTAGAAGATGAATTCAGGCACTTTCTTCAATAAACTAATTAAGGCTATTCCTTTGAAGAGCTGTAGA  
ACTGGATTCATTTTAAACCATTTTCACTAGTTTCAAAAGTAAATCTCTGATTGATTTTAAATGCGTCTTTGA  
AGAATTTCATATTAAGTAGTTTACAGATCTTATAAGGTGTTTATATATTAGAAGCAATTAATAATCACTCTG  
TGATTTCTGAACATAGGTGCTAAATCAGAGAAATGGAAGTGAAGTGAAGTATCTCTGTTGTCACTCGCATTC  
AATTTTCTCTTTGTTTGTGTCAGGTGTCATTTGAATATGTCTGTTCTATAAATAAATTTTAAAGATAA

09978192-101501

## FIGURE 155

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLALLAALAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMDPVTEPPVTDPVY  
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYLK  
KHKLLPNOWSADQLYLETTGKSRTLQSGGLALLYGFLPDFDWKKIYFRHQPSALFCSCGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMCHFCNVSFPC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQITIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSSEHSVRILYNGVDVTFHTSF  
CQDHHKRS PKPMCPLENLVR FVKRDMFVALGGSGTNYDACHREGF

**Signal sequence:**

amino acids 1-18

0978192-101501

# FIGURE 156

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCCTTTTGAAGAACAGTACTGTGGA  
 GCTATTTAAGAGATAAAAAAGAAATATCCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC  
 GCCGCTGTTTCAACCAATCGGGGAGAGAAAAAGCGGAGATCTGTCTGCCCTTGCACGCGCTGAAGCACAAAGCAGAT  
 AGCTAGGAATGAACCATCCCTGGGAGTAGTGTGGAAACCAACGGAGGAGCTGTACTTCCCAACTGTGCCATTCTAT  
 GGGCAGAAGGATGCTTCTGACTTTCAGTGGTTAAGGCGAGAATTGAAAAATAATTCTGGAGGAAGATAAAGATTGAT  
 TCTCTGCGCAGCTGCACCGGGACTACAAAGGGCTTGTCTGTCTGGGAATCTCTCTGGGAGCTCTGTGGGAGAGCCG  
 ATGCACCCAGATACGCTATTTCAGTTCCGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGAGCT  
 GGGGCTGCGAGCCCGGGAGCTCCGGGAGCGCGAGTCCGCATCATCCCAGAGGTAGGACGACGCTTTTCGCCCCT  
 GAATCGCGCAGCGGGAGCTTGGTCAACGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTGT  
 TCAATTAATCTAGACAACTTCGATGGAGGATAAAGTGAAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA  
 CGCAATCGCGCTTACTTTCGTGAAAGTGAAATAGAAATAAAAAATTAGTGAAAAATGCAGCCACTGAGATGCGGTT  
 CCTCTACCCACGCTGGGATCCGGATATCGGGAAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA  
 CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCG  
 CGAAGAAAAGGCTGCTCACACCTGGTCTTACGGCTCTCGACGGGGCGACCCCGTGGCCACAGGCACCGCGCG  
 CATCCGCGTGTATGGTTCTGGATGCGACAACGACACCGCACCAGCGTTTGCTCAGCCGAGTACCCGCGAGCGGTTCC  
 GGAGATCTTGGCCTTGGGACGCGAGCTGTCTGTAGTCAACGCTACCGACCTGACGAAGGAGTCAATGCGGAAGT  
 GAGGTATCTCTCCGTATGTGGACGACAAGGCGGCCAAGTTTCAAACATAGATTGTAAATCAGGGAACAATATC  
 AACAAATAGGGGAGTTGGACACAGGAGTCAAGGATCTACAGAGTGAAGTGAACGAATGGATAATGACAGGATA  
 TTTCTGCGGCGAGGCAAGTCTGTACTGTCTGGAGCTGAACGAATGCCCGAGAAGTGGTCTTCACTCTCTCT  
 CGCCAGCTCGTCTCCGAAAATCTCCACAGGGGACATTAATTCGCCCTTTTAAATGTAATGACCAAGATTCTGA  
 GGAACACGACAGGACTGCTTTTCTATCAAGGAAATCTGCCCTTTAAATTTAGAAAAATCTTACGGAAATTACTA  
 TAGTTTACTGACAGACATAGTCTTGGATAGGGAACAGGTTCTCTAGTCAACAATCACAGTGAACCGGCATGACCG  
 GGGAACTGCCCTCTATCCAGGAAACTCATATCTCGCTGAACGTGGCAGACACCAAGCAACCCCGCGCTCTT  
 CCTCAGGCTCTTATTCCTCTATATCCAGAGAAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA  
 CGACCCCGAGCTGTGAAGAGAACGCCAGATCACTATTTCCTGCTGAGAACCACTCCAAAGGGGCAAGCTCTATC  
 GTCTTACGTTCCATCACTCCGACACTGGGTACTGTATGCGCTGAGCTCCTTCCGACTACGAGCAGTTCCGAGA  
 CTGTGCAGTGAAGTGTATGGCGCGGACACCGGCGACCCGCCCTCAGCAGCAAGCTGTCTGTAGCCTGTCTGT  
 CTGTGCACAGAACGATACTGGCCCGAGATCTGTATCCCGCTCTCCACGAGCGGTTTCTCATGCTGGAGCT  
 GGTCTCCCGCTCCGAGAGCCCGGCTACTTGTGTACCAAGTGTGTGGCGTGGACAGAGACTCCGCGCAGAACCG  
 CTGGCTGTCTACCGTCTGTCTCAAGGCGAGCGAGCGGGACTCTTCTCGTGGGTCTGCACACGGCGAGGTGG  
 CACGCGCGAGCCCTGTCTGGACAGAGACGCGCTCAAGCAGAGCTCTGTAGTGGCGGTCCAGGACACCGGCGAGCC  
 CCTCTCTCCGCACTGTACGCTCAACCGTGGCGTGGCGCAGCAGCATCCCCAAGTGTGGCGGACTCGGAGC  
 CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGTGTGTAGCGGTGGCGCGGTCTCTGT  
 CGTCTTCTCGGCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT  
 TTCAGGAGGCGGCTTGAACAGGACGCGCGCGCTCGCACTTTGTGGCGTGGACGGGCTGACAGTCAAGCTTCTGT  
 CTATTTCCACAGGTTTCTCAACCGGACTCGCGGAAGAGTCACTGATCTTCCCCAGGCCCAATATGACGAGA  
 CATGCTCTGACGAGGAGGCTTTGAAAAAGAGAGCCCTTTTGTCTGTCAAGTGATTCGGTATTTCTAAAGA  
 CAGTCATGGGTTAATTGAGGTGAGTTTATATCAAAATCTTCTTTTCTTTTAAATTTGTCTCTGTCTCCCAAGC  
 TGGAGTGACGCGGTACGATCATAGCTCACTGCGGCTCAAACTCTAGGCTCAAGCAATATCCCACTTTGCGCT  
 CCGGTGTAAACAGGACTACAGGTGCAAGCCACTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCT  
 CTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT  
 CAGGCGGCTGGATCACTGAGTTTGGAGTTTGTAGACCAAGCTGACCAACATGGAGAAACCCCGTCTATCTAA  
 AAAAAATACAAATATAGCCGGGCGTGGTGGTGCATGCTGTAACTCCAGCTACTTGGGAGGCTGAGTCAGGAGAT  
 TGCTTTAACTGGGAGGTGGAGTTGCAATGAGCTGAGATTGTGCCACTCCAGCTGGGCAACAGAGTG  
 AAACCTATCTCA

09978192.101501



## FIGURE 158

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTTCATGAGTGCCAAACCCATTTCGAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCTTGTTAGGTGGCAACTGGGTCCCTT  
ACAGCTGCCCCTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTTCAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCACCAAGTCCCCGAGAGAATTTCTTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGCACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCACCTCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACCTCT  
CTGGTTC

0975392-101501

## FIGURE 159

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL  
VGGNWWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPIVVQSIHPHCYNSSDVEDHNHDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENF PDTLNCAEVKIFPQKKCED  
AYPQGITDGMVCAGSSKGDATCQGDSSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

### **Important Features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 51-71

#### **N-glycosylation site.**

amino acids 110-113

#### **Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

#### **Tyrosine kinase phosphorylation site.**

amino acids 182-188

#### **Kringle domain proteins motif**

amino acids 205-217

0970759.11504



# FIGURE 160

GGCGCCGGTGACCCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCCTGCGCGCCCGGCCCGC  
CGCGCCGCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCGGGCCCGCGCCCGC  
GCCCGCGCCAGGTGAGCGCTCCGCCCGCGCGAGGCCCGCCCGCCCGCCCGCCCGCCCGC  
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCTCGCGCTCAAACCACCTGATCCATAAAAC  
ATTTCATCTCCCGGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCCGCCCGCCCGCTCG  
CCCTGTGCGCCCTGCCGCGCCTGCGCACCCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGCGCGGCCCGGGCCGGGCGGTAGCGCGCGCGCTGGA  
TGGGACCCCGCGCGGGGAGACGGGCGCCCGCCCGAAACGACTTTCAGTCCCGGACGGCG  
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCGAGGCTTGGCAGGTGGCAGCCCCATGCCAGGTGCTGCGTATGCTACAATGA  
GCCCAAGGTGACGACAAGCTGCCCGCCAGCAGGCGCTGCAGGCTGTGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCTGTCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCTGCCGCAACCTCACCATCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC  
GGCTGCTTCACTGGCTTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTGTGTGGACCTGCGCATTTCCACGGCTGGGCGCGCTACACACGCTGCACCTGGACCGC  
TGCGGCTGCGAGGCTGGGCCCGGGGCTGTTCCGGCGCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCTGATGACACCTTCGCGAGACTGGGCAACCTCA  
CACACCTCTTCTGCGCGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCGCTGGGCTG  
CACAGCTCGACCGTCTCTACTGCAACGAGAACCGCGTGGCCCATGTGCAACCGCATGCCCT  
CCGTGACCTTGGCCCGCTCATGACACTCTATCTGTTTGCCAAACATCTATCAGCGCTGCCCA  
CTGAGGCGCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCGGGGCAAGCCACTCTGGGCTTGGCTGCAGAAATTCGCGGGCTCCTCTCCGA  
GGTGCCTGCGAGCTCCCGCAACGCTGGCTGGCCGTGACCTCAAACGCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGAACGGCAGGGCCAC  
GATGAGGAGCCGCTGGGCTTCCCAAGTGTGCCAGCCAGATGCCGCTGACAAGGCGCTCAGT  
ACTGGAGCCTGGAAGACCACTTCCGCGAGGCAATGCGCTGAAGGGACGCTGCCGCGCGGTG  
ACAGCCCGCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCTTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGGCGCCGAGGGCTCCGAGCCACAGGGTT  
CCCCACCTCGGGCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGAGCCACT  
GCCGCTGGGCCAGGCAGGCAGCGGGGTGGCGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCTCACCTGCAGCTCACCCCGCTGGGCTGGCGCTGGTGTGTGGACAGTGTCT  
TGGGCCCTGCTGACCCCGAGCGGACACAAGAGCGTGTCTCAGAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCGCCGAAGCCAGCGGGCGGCCGACCCGTTGGGGCAGGCCAGGCCAG  
GTCTCTCCCTGATGGACGCTTCCGCCCCGCCACCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGCGCGCAGCGTTTGTTCAGAAGCGCGCTTCCACCCAGATCGCGGTATATAGAGAT  
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTTTTTCTTAAA  
AAAA

09978192.101501

## FIGURE 161

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184  
><subunit 1 of 1, 473 aa, 1 stop  
><MW: 50708, pI: 9.28, NX(S/T): 6  
MKRASAGGSRLLAWLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIPAASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDP  
TFHGLGRLHTLHLDRCGLEGLGGLFRGLAALQVLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLHQNVRVAHVHPHAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRLNDNPWVCDRCARPLWAWLQKFRGSSSEVP CSLPQRLAGRDLKRLAANDLQGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDAAADKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDESGSGALPSLTCSLTPLGLALVLWTVLGPC

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Leucine zipper pattern.**

amino acids 135-156

#### **Glycosaminoglycan attachment site.**

amino acids 436-439

#### **N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

#### **VWFC domain**

amino acids 411-425

00970169-701501

## FIGURE 162

GGAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC  
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCAAGCCCTCAGATACCTGGGGACTTTAC  
AGTCCCACAGAACCCGCTCCAGGAAGCTGAATCCAGCAAGAACATGGAGGCCAGCGGGA  
AGCTCATTTGCAGACAAAGGCAAGTCTTTTTCTCTCTTTTGGGCTTATCTCTGGCG  
GGCGCGGCGGAACCTAGAAAGCTATTCTGTGGTGGAGGAACTGAGGCGAGCTCCTTTGTCAC  
CAATTTAGCAAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTTAGGGTTG  
TTTCCAGAGGGGAACAACTACATTTGCAGCTCAATCAGGAGACCGCGGATTGTGTCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGCGGTACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
GTTGCTAGAGAGTCCCTTCGAGTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAGTATCAGAGAGCAGTCTCTCTGGG  
ACTACGTTTCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAACAAATATTGAGAACTA  
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAACGCAGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGTCTGGACAAAGCGCTGGACCGAGAGGAAGAGCTGAGCTCAGGTTAAAC  
CTCACAGCACTGGATGGTGGCTCTCCGCCACAGATCTGGCACTGTCTCAGGTCTACATCGAAGT  
CCTGGATGTCAACGATAATGCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG  
AGGACAGTCCGGTAGGCTTCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTCT  
AACCGAGAGATTTCCTATTCACTTTTCCAAGCTTCAGAAAGATTGGCAAAAACCTTTAAGAT  
CAATCCCTTTGACAGGAGAAATTGAACTAAAAAACAACCTCGATTTGCAAAAACCTTCAGTCTCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACTTTTCTGGAAATGCAACCGTTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT  
ACCTGAGAACCGCGCTGAAACTGTGGTTGCATTTTCAGTGTTCAGATCTTGATTTCAGGAG  
AAAATGGGAAAATTAGTTGCTCCATTTCAGGAGGATCTACCCCTTCTCCTGAAATCCGCGGAA  
AATTTTACACCTACTAACGAGAGAGCACTAGACAGAGAAAGCAGAGCGGGAATACAACAT  
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGGTG  
TGATCGCGATGTCAATGACAACGCTCCCGCTTCACCCAAACCTCTACACCCGTGTTCTGTC  
CGCGAGAACCAACAGCCCCCGCTGCACATCCGCGAGCGTCAGCGCTACAGACAGAGACTCAGG  
CACCAACGCCCAGGTCACTACTCGCTGCTGCCGCCAGGACCCGCACTGCCCTCACAT  
CCCTGGTCTCCATCAACGCGGACAAACGCCACCTGTTGCGCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGGTTCCAGTTCGCGTGGGCGCTTCAGACCAGGCTCCCGGCGCTGAGCAG  
CGAGGCGCTGGTGCGCGTGGTGGTGTGACGCGCAACAGCAACTCGCCCTCTGTGCTGTATCC  
CGCTGCAGAACGGCTCCGCGCTCTGACCCAGCTGTTGCCCCGGGCGCGCAGCGGGGTAC  
CTGGTGACCAAGTGGTGCGGTGGAGCGGCACTCGGGCCAGAACCTGGCTGTGCTGTACCA  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCACAATGGCGAGGTGCGCA  
CCGCCAGGCTGCTGAGCGAGCGCAGCGCGCCAAGCACAGGCTGGTGGTGTGCTGGTCAAGGAC  
AATGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCTGGTGGACGGCTTCTC  
CAGCCCTACCTGCTCTCCGAGGCGCGCCCGACCCAGGCCAGGCCGACTTGCTCACCG  
TCTACCTGGTGGTGGCGTTGGCCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGTCTCCTGTT  
GTGGCGGTGCGGCTGTGTAGAGGAGCAGGCGCGCTCGGTGGGCTGCTGGTGGTCCCGA  
GGGCCCCCTTCAGGGGACTTTGTGGACATGAGCGGCAACAGGACCCCTATCCGAGAGCTACC  
AGTATGAGGTGTGCTGCGCAGGAGCTCAGGACCAATGAGTTCAAGTTCTCTGAAGCCGATT  
ATCCCCAACTTCCCTCCCCAGTGCCTTGGGAAAGAAATACAAGGAAATTTACCTTCCCCAA  
TAACTTTGGGTTCAATATTCACTGACCAATAGTTGACTTTTACATCCATAGGTATTTTATTT  
TGTGGCAATTCCATGGCAATGTTTATTTCCCAATTTGTGTGTATGTAATATTGTACGGAT  
TTACTCTTGATTTTCTCATGTTCTTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
CCTGGTCTT

09978192.101501

## FIGURE 163

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLGLSLAGAAEPRSYSVVEETEGSSFTNLAKDLGLEQREFSR  
RGVVRVSRGNKLHLQLNQETADLLNEKLDREDLCGHTEPCVLRQVLLESPPFEFFQAEQLQV  
IDINDHSPVFLLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFVLVVKVSATDVTGTVNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAFEVTMSAFTSPIENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLKSAENFYTLTTERPLDRESRAEYNITITVTDLGTPLITQ  
LNMVTLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYELQGFQFRVGASDHGSPALSSALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAEPGYLVTKVVAVDGDSGQNAWLSYQLLKATELGLFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYPPLPEAAPTQAO  
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLDMSGTRT  
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

amino acids 685-712

#### **Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

#### **ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

#### **N-glycosylation site,**

amino acids 418-421, 436-439, 567-570 and 786-789

0976192-101501

## FIGURE 164

ACCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCCACGCGTCCGCGCGTAGCCGTGC  
GCCGATTGCCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCGCGTCAT  
GCGGCTCCTCGGTGTTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGCGCTGG  
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAAGCGATCACATGGTGATGCTGTCTG  
TGATTCTCTGGGGAAGCTGAGGACAAAGTGAGTTGAGGCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCGAGAGAGCCTTTTCTCTGTGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCTGTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCCTAGC  
TGTTCCCTAATATTTTATTATTTCAGGAGCTAAACCAATGGCCAGATTTAATCATAAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAAAATAGGCCCTCTTCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTGTATTTTCTTATTCTTTTAAATTAGTTTTATTATGTATGCTACCATTGAA  
CTGAGAGTATTCGGTGGCTAATTCCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTGTGACTTGAACTTCAGGCAGATTAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

0978192.101201

## **FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333  
><subunit 1 of 1, 360 aa, 1 stop  
><MW: 39885, pI: 4.79, NX(S/T): 7  
MVPAAGRPPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDPMGQDRAAEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC  
NVRESLFLSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMPARFNHTDRTLLETLKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFLSFFLISFIMYATIRTESIRWLIPGQEHEVE

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Transmembrane domain:**

amino acids 321-340

#### **Homologous region to dilsufide isomerase**

amino acids 212-302

#### **N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

#### **Thioredoxin domain**

amino acids 211-227

097316.11511

## FIGURE 166

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCTCTGCGCTCGCACTGCTGCCTGGGCTCGGCGCGGGGCTCTTCTCTC  
TTTGGCCAGCCCGACTTCTCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCCAACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCTCTGTGCTCGCTCTTCGCCCCGCTGCTGCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAGGTGAAGGACCGCTGCGCCCCGGTTCATGTCCG  
CCTTCGGCTTCCCCTGCGCCGACATGCTTGAGTGCACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAAATAAAATGATGATGACAACGACATAATGGAACCGCTTTGTAAAAATG  
ATTTTGCACTGAAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACAAAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTA  
GTCCCGGCATCCTGATGGCTCCGACAGGCCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC  
GGGATCTCAGCTCCCGTTCCTCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCCCCGAATCTGTAGAAATATTCAAACATAATA  
AAATCATGAATATTTTAA

0976352.101501

## FIGURE 167

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSAAGLFLFGQPDFSYKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKVEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLDETIQCHSLCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKKNKDDDDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETSKSTYKLNQVSRDLKKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQGGLVITSVKRWQKGQREFKRIISRIRKLQC

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

0973132-101501



[illegible]

GTGAGGCGCCGCGACCAATGCGCGGGCCGACGAGGCCGAGACGSGGTTGGCCGAGCCCCGGG  
 CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTCTGCTCGCGATC  
 AGCCTGTCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
 TGCTGAGGACTTGGTCTCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCTGTGG  
 TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGCTGGGCTCCGTGCGGGC  
 ACCATCTCTGGGTGCGTGGCTGAACTTTGCGGGAGTGTGCTACGCATGGTGCCTGTCATGGT  
 TGTGGGACCCAAACCCATTTGCCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
 AGAGCCTGGTCACTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGACCAGCGA  
 GCCACGGCCAACATGCTCGCCACCATGTCGAACCCCTGGGCGTCTTGTGGCCAATGTGCT  
 GTCCTTGTGCTGGTCAAGAAGGGTGAGGACATTCGGTTAATGCTCGGTGTCTATACCATCC  
 CTGCTGGCGTGTCTGCTGCTGCTCCACCATCTGCGCTGTGGAGAGTGTGCCCCCCACCCCG  
 CCTCTGCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCTTGGATGGGCTCAAGCTCAGCTC  
 CATGTGGAAAGGGCCCTATGTCACTCTGGCTGTGTAGTTTGGGGGGAATGATCGGGATCTCTG  
 CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
 GGCTCTGTGGCGCTCTCTTCATACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCTTA  
 TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
 CCTGCGTGCCCTTTGCGCTGGTGTCCAGCTGCAGGGACAGACCCTTGCCTTGGTGTCCACC  
 TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTGCA  
 GTGTTCTTCCCCTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
 AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGCTCCTTG  
 TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCCTGTCTGCTGATGGCCGG  
 CCTGTGCACCTTCTTCAGCTGCATCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
 AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
 GGTGTGGACCGAGGGGGGAGCAGGAAGGGCTGGGGTCTTGGGGCCACGACAGCGACTCCGGA  
 GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCGGGAGCCCCACCCAGCCT  
 GCCACCGAGCGACTCCCCGTGCGCAAGGCCCAGCAGCCACCGACGCGCCCTCCGCCCCGGC  
 AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
 CTCCTCCCCTGGGTGATCAGCTAGCTCAGCGCCTTTAGTCCAGGTTGCCCGCCACATCGA  
 TGGAGGCGAAGTGAACATCTGGTCCACTCGCGGGGGGGCGAAAGGGCTCCTTGCGGGCT  
 CCGGGAGCGAAATTACAAGCGCGCACTGTAA

## FIGURE 169

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFGAGSVLRMVPCMVVGTQN  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFFEHQRATANMLATMSNPLGVLVANVLSFVLV  
KKGEDIPLMLGVYITIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFALLEQILCASGHSSGSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLFSLACVPFALVSQQLQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAEIGILMLAMTALTVRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

### **Important features:**

#### **Signal peptide:**

amino acids 1-44

#### **Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

#### **N-glycosylation site.**

amino acids 40-43 and 43-46

#### **Glycosaminoglycan attachment site.**

amino acids 468-471

097819-101502

# FIGURE 170

GTCCCACTCATCTGCTCAACTGGGGTCAGGTCCCTCTTAGACACAGCTCTTGTCCATCATTTGTCTGAAGTGGACCAAC  
 TAGTTCCTCCACAGTAGGGGGTCTCCCTCGGCAATCTTGATCGGCGTTTGGCAATCTCAGATCGCTTCCAATGAAGA  
 TGGCCTTGCCCTTGGGGTCTCGTGTGTTTTCATAATCACTAATAGTGGACAGGCTGTGCGCGGACGCTCTGGGGG  
 AAGGAGCAGCGGGCTGATCAAGGCCATCCAGGAAACACTGAGGAGCACTGTGCGAGCTTGTGAAGAATCTAGTGGTT  
 TCTGAATCTAGGCCACTTTGGCGGTGAAGC**AT**GATGCAACTCTCGCAACTCTCTGCTGGGGCTTTTGGGGCCAGGTGG  
 CTACTTATTTCTTTTAGGGGATTTGTTCAGGAGGTGACCACTCTCAGCGTGAATATCCAAAGTGTTCAGAGAAAGTGCC  
 ATCTGTGTACAGTACGCTGTGCCGACAGTGGGATCCCTCGGACAGTGGCGAGGAGAGCGGAGCTCAAGCTGGGGCGCCTT  
 CCAGGTGTTTGCAGCTGCTCAGGCGCTCCCAATTACAGTGGACTCTGAGGAAAGGCTGTGCTCAGCAGCAGCAGCGG  
 GCTGGATTCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCTGGTTCCTTTGATGTGCTTGCACAGGGGATTT  
 GGCTCTGATCTCATGTGGAGATCCAAGTCTGGACATCAATGACCCAGCAGCCAGGTTTCCCAAAAGGCGAGCAGGGA  
 GCTGGAAATCTCTGAGAGCGCTCTCTGCGAAACCGGATCCCTCGGACAGAGCTCTTGACCCGACAGCAGCGGCT  
 TAAACCCCTGCACACTACACTCTGTCTCCCAAGTGAGCACTTTGCTTGGATGTCAATGTGGGCCCTGATGAGAC  
 CAACATGCAAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCAATTTTGTATCTGGTGTAACTGTC  
 CTATGCAATGGGAACCCGCCAAGTCAGGTACAGCTTGGTCAAGGTCAACGCTCTTGGACTCCAATGACAAATAG  
 CCGTTCGGTTTGTCTGAGAGTTCACTGGCACTGGAAATCCAAGAAGATGCTGACCTGGTACGCTTCTCATAAAAT  
 GACCGCCACAGACCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCTCAGTACAGACATGCTCTCCAGAGGT  
 GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTCGACCTTAGACTATGAAAGAACCC  
 TGCTTACAGGTGGATGTTCAGGCAAGGAGCTGGGTCCCAATCTTATCCAGCCCATGCAAGGTTCTCATCAA  
 GGTCTTCGAGTCAATGGAACTTTTATGCTCTTGTCTATGGCAGATGACTTGGATTCAGGACCAATGGTTTGGTCCA  
 CTGCGTCAAGCAGGAGAGCTGTGGCCCAATATCACTTCTGTAGGCAAGCAGGAGCTTCCAGCTTCCAGCAAGCT  
 CACATCTGGAACAGAGCAGCTGTGGCCCAATATCACTTCTGTAGGCAAGCAGGAGCTTCCAGCTTCCAGCAAGCT  
 AGGCAAGAAACAGCTCAGCACTCAGATCTCAGATCACTGACATCAACGACAAATGCACTTGTGTTGAGAAAGCAGGATGA  
 AGTCTTCCAGCGGGAAACAACTATGCTCTTCTCACTTCAATTACATCAAGGCTCATGATGAGCAGCTTGGGAT  
 TAATGGAAAGCTCTCATACCGCATCCAGGACTCCAGGACTCCGAGGATGAGGAGTGGCCCGGCTTGTGATTCAGGTGAT  
 GGTCTACTGCTCAGAGTCTCAGTAACTATGAAGAGATGGCCCGGCTTGTGATTCAGGTGATGCGCAGAGCAGCGG  
 GCAACCCATGCTTGCATCCAAGTGTCTGTGTGGGTGAGCTTGTGATGCCAATGATAATGCCAAGAGGTGGT  
 CCAGCTGTGCTCAGGATGGAAAGGCCAGCTCTCCGTCTTGTGAATGCTTCCAGGCCACTGCTGCTGGTGGC  
 CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACTCCACTGAGGCCACTGCTGCTGGTGGC  
 CTTTTTGAACAACCTTGTGGCAAGAGATGACAGACTCGGGGGCAATGGAGGCCCTTACAGCATCCGCAATGG  
 AAAATGAAGCCCACTCTTCACTCTCAACCTCTATACGGGCACTGTTTCTGCAATGTCAACATGCCAGCAAGCT  
 CATTTGGGATGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAAGGAGGCCCTTACAGACCCGAGCCTGTT  
 GAGGCTCATGTTTGTCAACAGTGTGGACCACTGAGGAGCTCAGCCCGCAAGCCTTGGGGCTTGAGCATGTGAT  
 GCTGACGCTGATCTGCTGGCTGTACTGTGGGATCTTGGGTTGATCTTGGCTTGTTCATGTCCATCTGCGG  
 GACAGAAAGAAAGGACCAACAGGGCTTACAACCTGTGCGGAGGCGGAGTCCACTACCGCAGCAGCCCAAGAGCC  
 CCAGAAACCACTTCAAGAGGACAGACTCCACTCTGCTGTGCTCAGGGTTCAGGCAAGTGAAGCTTGTGATG  
 CGGGCAGTCCCAAAAGATGTGGACAGGAGGCGATGATGGAAGCAGGCTGGGAGCCCTGCTGACGGCCCCCT  
 CCACTCCACCCGACCTGTACAGGACGCTCGTAACTCAAGGACCAAGGAGACACTGCGCCACTTGTGATG  
 GCTGCAAGCAGCGTCAACTCTCTTTTCAACCATCCAGGCAAGGAATGCTTCCCGGAGAACCTTGAACCTTCC  
 CGAGCCCCAGGCTGCCACAGGCGAGCCAGTTCAGGCTCTGAAAGTTGCAAGGACGCCCAAGGAGGCTGGC  
 CTAGGACCAAGGCGAGTGAAGGAGCCCAAGAGGCGCCAGGCTCTCTGCAACCTGAGACCGGACGACATCT  
 CAATGGCAAAAGTGTCCCTGAGAAAGAACTCAGGCGCCGCTGCTCAGATCTTCCGAGAGCTTGTCTGTGGC  
 TGCTTCTGCGCGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATCTCTCTCTGCTGCAAGAACTTCCAGGCTGCT  
 GTCTTCTGTGATCAGGCGCAATTCACGCCAAACCAACCGAGGAAATAGTACTTGGCCAAAGCCAGGAGG  
 CAGCAGGAGTCAATCCAGACACAGATGGCCCAAGTGAAGGCTGAGGCGCAGACAGCCAGACAGGAGGAG  
 AGGCGCTTGTGATCTTGAAGAGGACTCTCTGTGAAGCAACTGTGAAGAGAGAGCTGTCAAGTCTGTGTGACCC  
 CAGCAGAGTGTGCGCTTGACCGGCTGAGCGGCCCTGACCGGCTGGATGGCGAGACTCTCTTGGCCCTTAC  
 CCAACTACCGTGCAATTTGATCTCCCGGATGCTGACGACCGAGGAGGAGGACTTCCAGACCTTCCG  
 CAAGCGAGGACCAAGAGCTGAGGCCCAACAGGCAAGGAGGCTGGCCAGCACTTGTCTGCGAGATGAGCTCACT  
 GCTGAGATGTGCTGTGAACAGGCTCCAGCATGCGCTGGAGGCGCTTCCAGAGGCTGCGCGGCTCTCGGT  
 CTGCGGAGGACCTTCACTTGTAGCTTGGCCACAGTGCAGCTCAGGCATGAAAGTGCAGGAGGCCACCGGTGG  
 AAAGAGCGGGGCTGAGGCGCAAGCAGAGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC  
 CTGATCTCAGAAACCAAGGGGCTGAGGATCTGTGACACAGCTGGTTTCTTAAATCTTGTAACTCACTAGCTAG  
 CGGCGGCTGAGAATTTAGGCTGACTGTGCTACCCCAAGGAGGACAGGAGCCAGGACCAAGCAGCTGAC  
 GCTCAAAGCAGCCCTTTGTAAGCAGCTCTGATGCTTTTGGAGGACAGGCGGTTTGGCTGAGATATGTTGT  
 TCTTGCAGAAACATATGTGGAGCACAAAGGCTCAGTCTCTCCGAGAACAGATGCCAAGGATATCAGGACAGG  
 AAAGGCTGGCTTCTTGGGTAGCAAGAGTCAGGAGTGGGGGCTGTACCTGGGGTGGCAGGAATGCTCTTGAACCTAT  
 CAATAAAGGAAAGCAGTAAATAAAAAAAAAAAAAAAAAA

09978192.101501

## **FIGURE 171**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331  
<subunit 1 of 1, 1184 aa, 1 stop  
<MW: 129022, pI: 5.20, NX(S/T): 5  
MMQLLQLLLGLLPGGYLFLLLGDCQEVTTTLTKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAPQVLQLPQALPIQVDSEGLLSTGRRLDREQLCRQWDPCLVSFVDLATGDLALIHVIEIQ  
VLDINDHQPFRFPKGEQELESSESASLRTRIPLDRALDPDTGPNLTHTYTLSPSEHFALDIVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESS  
LALEIQEDAAPGTLIIKLATATDPDQGPNGEVEFFLSKHPPEVIDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNPPIPAHCKVLIKVLVDNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLTLLAQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSSTRENNLPSLHLITIKAHADLGINGKVS  
YRIQDSPVAHLVAIDSNTEVTQAQRSLNYEEMAGFEFQVIAEDSGQPMCLASSVSVMVSLDDA  
NDNAPEVVPVPLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTTPPLATHSSRPFLTTT  
IVARDADSGANGEPLYSIRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSDVHRLDSARKPGALSMSMLTVCICLAVLLGIGFLILALFMSICRTEK  
KDNRAYNCREAESTYRQPKRPQKHQKADIDLVPVLRGQAGEPCEVQGSHKDVDKEAMMEA  
GWDPCQLQAPFHLTPTLYRTLNRQGNQGAPAESREVLQDVTNLLFNHPRQRNASRENINLPEP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSSEAPQRPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAFAERNPVEELTVDSPVQIQISQLLSLLHQGQFQPKPNHRGNKYLAKPGGS  
RSAIPDPTDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTNTYRDNVISPDAAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEMLELQRSSMPVEAASEALRRLSVCGRTLSLDLATSAASGMKVQCDPGGKTGTEGKSRGSS  
SSSRCL

### **Important features:**

#### **Signal peptide:**

amino acids 1-13

#### **Transmembrane domain:**

amino acids 179-739

#### **N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

#### **Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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## FIGURE 172

CGGACGCGTGGGCGGACGCGTGGGGGAGACCGCAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCAATTTCTTGCAACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATCTGCTGATCCTGGTTCATGGTGCCCTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACCTAGGAGATCCCTTTCCTATTCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTTCTGGATTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT  
CAGGAATGTGACTGACACGGATATTTCTAGCCCTGGAACGGCGACTGTGTCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCAGGAGAACAAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTACCACTTCAGCATCAGG  
AAGTGAAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAAATATTTTAAATTTTCTGGTTACTTTTTCTCTATTTTACTGTGTTTGGAAAAATTT  
CATGGCTACCATCAATATTTGTTTTGATCGAGTTGGGAAAACGGATCCTGTCAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTGGTCCCAACACATT  
TCCTTCATTCTGTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCCTCCAATGTCAATGTCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCTCTGTGCTGCTGATCCGAATGAGTATGCCCTTTAGAA  
TACCGCACCATAAATCACTGAAGTCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT  
TGATGTGATCTTCTGGTCAGCGCTCTCTCTAGCATACTCTTCTCTATTGGGCTCAGAAAC  
AGGCACCAGAGAAGCAATGGCACCTTGAACTTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAAATTTAGATATAAGAGGGGGGAAAAATGGAACAGGGGCTGCATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCTTCCCCGTGAGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAAGAAACTAA  
AGGTGAAAAATACACTGGAACTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTAAGGTTTCATGGAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAAATCAGAGACTGTAACAAAAAAGGGCGGCGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCACTTGTATTATGCAGCTTATAATG

## **FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYAIRQYVVQVIFSVTFAFSCTMFELIIFEI  
LGVLNSSSRYPFHWMNLCVILLILVFMVPPYIGYFIVSNIRLLHKQRLLFSCLLWLTFFMYFF  
WKLGDPPILSPKHGILSIEQLISRVGVIGVTLMALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMKSVTTSASGSENLTLIQ  
QEVDALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDPVTRGIEITVNYLGIQFDVKFWSQHISFILVGLIIVTSIRGLLITLTKFFYAISS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

#### **N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

#### **Eukaryotic cobalamin-binding proteins**

amino acids 151-160

09070192-101501

## FIGURE 174

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCGANACTATTTTTTGGATTGGGTGGCTTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTINTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAAACAACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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## FIGURE 175

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCTTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTTNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCAATTTCTTGCAACCATGTTTGAGCTCATCATNTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTCATGGTGCCPTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTC

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# FIGURE 176

CTGCGCAGGGATCGTCCATGCGCGGGGCTCGGAGCGGACCCCTTGGGGGGCTCGGGAGTTTGCTACCTTTT  
 TGCTCCTCTGCTGCTGCAACTGCTCTTCTCACGGGCTGTCGCTTCAACTCTGGAGCTGATGGGTGCTTTCGCGCA  
 GGAGGGCGAGCGAGCGAGCTCTTTCGGCTTCTCTGTGGCCCTGACCGGAGTGTAGCGCCCGAGCCAGAGCTG  
 GCTGTCTGTGTGGTGTCTCCCAAGGCGCTTGCTCTTCTCTGGGAGCAGCGCGAATCGCATCTGGAGGCTCTTCTGCTT  
 CCGGTGTGCGCTCGAGGAGACTGACTGTCTCAGAGTGGACATCGACCGAGGAGCTGATATGCAAAAGGAAAGCA  
 GGAGAACAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGGCAAGATGTTTACCTGTGACACCGATA  
 TGAGGCAAGGCAAGGAGTGAGACGATCTGGAGACGGGATATGATTGGTCGTGCTTTGTGCTCAGCGAGGA  
 CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAAATGGAAGTTCTGTGAGGGAGCGCCCCAAGGCCATGAACAATT  
 TGGGTTCTGCCAGCAGGCGACAGCTGCGGCTTCTCCCTGATAGCCATGACTCCTCTTTGGGGCCCCAGGAAC  
 CTATAATTGGAAGGGCAGGCGCAGGGTGGAGCTCTGTGCAACGGGCTCAGCGGAACTGGCAACACTGGACGACGG  
 TCCTTACAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCGGTCCCTGCCAACAGCTACTTTGGTCT  
 CTCTATTGACTCGGGGAAAGGTCTGGTGGCTGCGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAAACCA  
 CAAGGGTGTCTGTGCTCATCTCGCGCAAGGACAGCGCCAGTGCCTGGTGCCCGAGGTTATGCTGTCTGGGGAGCG  
 CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGTATGGCTGGCCAGACCTGATAGTGGG  
 TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTCTGTATGTGACTTGAACAGGGGGGTCACTG  
 GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTTCGGGATCAGCTGGCTGTCTGCGGGGA  
 CCTCAACCAAGATGCTTTCCAGATATTCAGTGGGTGCCCTTTGATGGTATGGGAAAGCTTTCATCTACCA  
 TGGGAGAGAGCTGGGGGTTGTGCGCAAACTTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCTCAAGAGCTTCGG  
 CTACTCCCTGTTCAGGAGCTTGGATATGATGGAACCAATACCTGACTGACTGTGGTGGGCTCCCTGGCTGACAC  
 CGCAGTGTCTTCAGGGCGAGCCCATCTCCATGTCTCCCATGAGGTCTCTATTGTCTCCACGAAGCATGCACT  
 GGAGAGCGCCAACTGTGCTGCGGGCCACTCGGTCTGTGTGAGCTTGTGTTGAGCTACATTGCACTGCCCTCC  
 CAGCAGCTATAGCCCTATCTGGGCGCTGGACTATGTGTAGATCGGGAACAGACCGAGGAGCTCCGGGGCAGAGT  
 TC00CGTGTAGCTTCTGAGCGGTAACTTGGAGAACCAGCAGCAGGCTCGGGCAGCGTGTGGCTGTGAAGCA  
 CCAGCATCAGCAGGATCTGTGGAGAGCCCATGTTCCAGCTCCAGGAAATGTTCAAAGCAAGCTTCGGGCGAATTGT  
 AGTAGACTTTGTCTACAGTCTCTCAGACCCCTCGGCTCCGGGACAGGCTCTGGCCAGGCTGCTCTCAGTGGC  
 C00CATCTCTAATGCCCAACGAGCCAGCACCAGCGGCGAGAGTCCAATCTCTGAAGCAAGGCTGTGTGGAAGA  
 CAAGATCTCGCAGAGCTTCTGAGCTGTGTCACGCGCTTCTGTATCCCGGCTCAGCGACAGGAAATCTCAACC  
 TCTGCCCATGAGATGGAATGGAACCAACAGCCCTGTTTGCATGTGGGCAAGCTCATTTGGCTCGGAGCTGGT  
 GGTCAACCACTGCCATCGGAGCCAGCCAGCCCGAGGCTGATGGGATGATGCCCATGAAGCCAGCTCTGTGT  
 CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCGCTGGACCTCGCGAGAGAACCATCTGCTCTGTCCAA  
 TGAGATGCTTCCATGTTGAGTGTGAGCTGGGGAACCCATGAAGAGAGGTGCCAGGTCACTTCTATCTCAT  
 CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAACCTGAGGTAGAGCTGCTGTTGGCCAGATCAGTGAAGA  
 GGAGCTGATCCAGCTCTGACAGAGCCGCTGTCTTATTGAGCTGCCACTGTTCATTGAGGAAATGGCCATTCC  
 CCAGCACTCTTCTCTCTGGTGTGGTGGGGGGGAGAGAGCCATGCACTGTGGCGGATGTGGGCGAGCAAGGT  
 CAAGTATGAGGTACCGTTTCCAACCAAGGCGAGTGCCTCAGAACCTTGGGCTTGCTCTTCAACATCATGTG  
 GCGTCATGAGATTGCCAATGGGAATGTTTGTCTGTACCAATGCGAGGTGAGCTGTGGGCGAGGCGGGGCTGG  
 GCGAAGAGGGCTTTGCTCTCCAGGCGCCAACTCTCCACTGGATGTGGAAGTGGGATAGGAGGCGGGCGGA  
 GCTGGAGCCACTGAGCAGCAGGAGCTGTGAGCGCAGGAGCCAGCATCTGTGGTGGCCATGTCTCTGCG  
 TGAAGAAGAAAACATCACCTGGACTGCGCCCGGGGCGAGGCAACTGTGTGGTGTCTGAGTGCCTCACTCTA  
 CAGCTTTGACCGCGGGCTGTGCTGATGTTCTGGGGCGTCTCTGGAACAGCACTTTCTGGAGGATGACTCAGC  
 TGTGAAGTCCCTGGAAGTATTGTCTGGGCGCAACATCAGAGTGAAGTCTTCCATTAAGAACTTGTGCTCGAGA  
 TGCCCTCCAGACTCCAGTGTGATGATACTTGGACACTGGCTGTGGTGGAGGAGGAGTCCCTGGTGGGT  
 CATCTCTGCTGTGATCTGCTGGCTGTGCTGTGCTAGCACTGCTGGTGTGCTCTCTGTGAAGATGGGATTTCT  
 CAAACGGGCGAAGCACCCCGAGGCAACCGTGGCCAGTACCATGCGGTGAAGATCTTCTGGGGAAGA.CCGACGA  
 GTTCAAGGAGGAGAAGACGGGCAACATCTGAGGAACAACTGGGGCAGCCCCGGGCGGGAGGGCCGGATGCA  
 C00CATGTGGGCTGACCGGCTATCCGAGCTGGGCGCGATGGGCATCCAGGGCGAGGCAACGCGCTAGGTTC  
 CATGTCCAGCTGGCTGCTGAGCTGCGCTGCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGTAGAGT  
 GGCGCTGCTGGTGTGCTATGAGTTTGGCAGGATCGCTTCTCAGGGGCAAGACCTTCCACCAACAGGAAC  
 TCCCTCCACCAAGCTTCCCTTGTAGATGTGTGAGATGAGAGTGGGTAATCAGGCAAGGCGCATGGGGTAGGG  
 TGAGAAGCCAGGGTGTCTGATGCAAGAGTGGGGAGAGGGGCTAATCCCTTCTTCCATCTCACTCTGCT  
 GTAACAGGACCCAGGACTGCTCCCTCCCGGAAGTGCCTTAACCTAGAGGGTGGGGAGAGGTTGTGTCACTGA  
 CTCAGGCTCTCTTCTAGTTTCTCCCTCTCATCTGACTTGTGCTGCCATGATCTAGTGGTTTCTGTGT  
 TTGCTCTATTATTAATAAATATTTGAGAACAAAAA

03978196.101501

## FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL  
GVSVRSQGPGGKIVTCAHRYEARQRVDQIILETRDMIGRCFVLSQDLAIRDELDDGGEWKFCG  
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGATARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLI PVPANSYFGFSIDSGKGLVRAEELSFVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYS LAVADLNSD GWPDLIVGAPYFFERQEELGGAVVYVYLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGDNLNDGFPDIAVGAPFDGDGKVFIYHSSSLGTVAKPSQVLE  
GEAVGIKSGFYSLSGSLDMDGNQYPDLLVGS LADTAVLFRARPILHVSHEVS IAPRSIDLEQ  
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRLRGQVPRVTFLSRNLEEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTPRLRRQAPGQGLPPVAP  
ILNAHQSTQRAEIHFLKQCGGEDKICQSNLQLVHARFCTRVSDETFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSDPAQPAQADGDDAHEAQLLVMLPDSLHYS GVRALDPAEKPLCLSN  
ENASHVECELGNPMKRGAQVTFYLI LSTSGIS IETTELEVELLATISEQELHPVSARARV  
IELPLSIAGMAIPQQLFFSGVVVRGERAMQSERDVGSKVKYEVTVSNQGGSLRTLGS AFLNIM  
WPHEIANGKWL LYPMQVELEGGQGPQGKGLCS PRPNILHLDVDSDRRRRRELEPPEQQEPGE  
RQEPMSGWWPVSSAEKKKNITLDCARGTANCVVFSCLYPSFDRAAVLHVWGR LWNSTFLEEY  
SAVKSLEIVIVRANITVKSSIKNLMRLRDASTVIPVMVYLDPMMAVVAEGVPWWVILLAVLAGLL  
VLALLVLLWKMGGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGITILRNWGS PRREGP  
DAHPIAADGHPHGLGPDGHPGPCTA

### Important features:

#### Signal peptide:

amino acids 1-33

#### Transmembrane domain:

amino acids 104-1062

#### N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

#### Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

09978192.101501

## FIGURE 178

CGGCGCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCAGCAGGAGCTGCGAGCACAGTGTGGCT  
CACAAACAGATGCTCAAGTGTGCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCACTCA  
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGCGGTCCGACGGCGGTAATTTTC  
TGGATGATAAAACAATGGCTCACCAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACCTTGGAGTCCAGGAAAACCCCTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AATAGAAATATCAGGCATGTGTCTTAGGAAAAAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCTTTCAGATAAGCCCACAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTTCAGGGAAGTGGCAAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAAGTGAA  
GTCAAAAACAAGAAGACAAAAACATTTGCTGAGGCCTGAGAGAAGCAGATTTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAAATATGACCT  
GCTATTGGACCAAGTCAGAGCTCAGAAGCATTACCTTGATAAAGATGAACAGTGTACCAAGG  
CATTTCTCAATTCTTGTGACACATACAAGGACAGTTTAAATATCTAATAATGAGTGGTGCTAC  
TGCTTCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAGAAGCTCCTAGGACAGTATATCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACAATATGTATGGCAGTGTGGACAGTGTCTGGTGTGTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTGACAGATTGTGCTATAGATTTTGAGATCTCCGAGAGATT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGATGAC  
CATGATGTATACATTGAGTTGATGACAGTTGAAATCAATAAAATTCACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAATATCTTCTCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTGTATAAATATTTGAAAAATGCAGCTAAAGTTATAGAAGTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTATATTCCTTACACAAAAAGAAAATACATATGCAGCTTA  
GTACAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAAATTTTCACGAGAACAACCTTTGT  
AAATCTTCCATAAGCAAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTGAAG  
ATAATTCTAAGTGAAATTTAAAAATAAATAAATTTTTAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAAATAAAAAA

00978192.101501

## FIGURE 179

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFDDQALDPAKDPCLMKKCSRHKVCIAQDSQTAVCISHRRLTHERMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQLNKKTKTLRPERSRFDTSILPI  
CKDSLGMWFMNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDDGYKPTQCHGSGVQCWCVDYRGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDDDDIMNDEDEIEDDEDEDEGDDDDGGDDHDVYI

### **Important features:**

#### **Signal peptide:**

amino acids 1-16

#### **Leucine zipper pattern.**

amino acids 246-267

#### **N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

#### **Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

00978192.101501

# FIGURE 180

CAGACTCCAGATTTCCTGTCAACACAGGAGGATCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC  
 CTCCTTCAGCCGGGATCGCCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCTTCTTGCC  
 GCTTGCTCCGGTGCTGCTGGCTGGGCGGCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCTCTT  
 CCGCCCGGCCAGAAAGAGTGCTTCTACAGCCCATGCCCTGAAAGCGCTCGCTGGAGTTCAGATACCAAGTTTAA  
 GATGGAGCAGGATTAGATATTGATTGATTTCCATCTTGCTCTCCAGAGGCAAAACCTTAGTTTGTGAACAAAGAAA  
 TCAGATTGGAGTTTCACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACTTCAGCACCATT  
 TCTGAGAAGTGATTCTTTTGAATTGATCTCTGGATAATATGGGAGAACAAGGACACAGAAAGAGATTGGAAG  
 AAATATATTTACTGGCACAAGATATTTGGATATGAAACTGGAAGACATCTCGGAATCCATCAACAGCATCAAGTCC  
 AGACTAAGCAAAAGTGGGCACATACAAATCTGCTTAGAGCAITGGAAGCTCGTGATTCGAAACATACAGAAGAAC  
 AACTTTGATAGAGTCAATTTCTGGCTATGGTTAAITTAGTGGTTCATGGTGGTGGTGCAGCCATTCAAGTTTAT  
 ATGCTTGAGAGTCTGTTTGAGATAGAGGAAAGTAGAATCTAAACCTCCAAACTAGAGTACGTAAACATTGGA  
 AATGAGGCATAAAATGCAATAAATCTGTACAGTCAAGACCAATTAATGGTCTCTCCAAATATTTTGGAGATATA  
 AAAGTAGGAAAACAGGTATAATTTTAAATGTGAAATTAAGTCTTCACCTTCTGTCGAAGTAATCCGTGATCCAG  
 TTGTACTTAAGTGTGTACAGGAATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT  
 TTTCTAACTTTGAAAATTTTGCNAATGCTTAGGTGATTTAAATAAGTATGAGTATGGGCCATAATTGCAACCC  
 AGTCTGTTTAAACAGGTTCTATTACCCAGAACCTTTTGTAAATGCGGAGTTACAAATTAAGTGTGGAAGTTT  
 TCAGTTTAAAGTTATAAATCACCTGAGAATTAACATAATGATGAGTATGGGCCATAATTGCAACCC  
 CTTTCTCTATTACATATGATCATCTCTCTATAATGTAAATGAATATAGCTTTGAAATACAATTAGGTTTGTG  
 AGATTTTATAACCAATACTCTTCAGTGTAACTATTAGCAGAAAGCATTAGTCTTTGACTTTGCTTACATCT  
 CCAAAAGCTGACATTTTCAAGTTCTTAAACACAAGTTACACTTACTAAATTAGGACATGTTTCTCTTTG  
 AAATAGAGAAATATAGTTTAAAGCTTCTCTCATAGGACACATTTCTTAAACCTTAACTAAAGGTAGGA  
 TTTTAAATTAAGTGTGAGGTAAATTAAGTTTATTTTAAATAGTATCTGTCAGTAAATATCTGTCAACAGTTAA  
 TAATCATGTTATGTTAAITTTAAACATGATGCTGATCTGATTAATCTACAGCAGTATGAAGAAATA  
 TTGCTAAATGATCTGGGCTCCATCAATAAATAATATCTCTTTCTGAGCTCAAGAAATATCAGAAACAGGAA  
 AGAATTTAGAAAACCTGTAGAAAACCTAATCCAAATAAAATCTCACTTAAGTAGAATATAAATAAATCAGGA  
 ATCTGACTGGCTCATCATGACCTCTACTCATAAACATAAATCAAAGGAGATAGTAATTTCCAGTTAGCTGGAAG  
 AAACCTTTGGCTGTAGGTTTATTTTCTACAAAGATTTCTGGTTGAATTAATTTTGTAAAGCAGTACATTTTATA  
 AAATGTAGCCCTACTGTAAAGTTAGCACTGGGTGACATAITTTTAAATTTTATTAACCAACTTTTAT  
 TAAATGGCCCTTCTGAACACTTTATTTATGATGTTGAAGTAAGGATAGAAACATAGACTCCCAAGTTTAA  
 CACTTAATGTGAATAACCCATATATACAAAGATTTCTGCCATCTAGCTTTTGAAGTCTATGGGGCTTCTAC  
 TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATATAATTTTAAAGTTATGCCCAITTTAATACGTTGTTAT  
 GACTACATTTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCTCAACAGGTTAGTATGCTGGAAT  
 CTTGATGAGCAATAATGATAACAGAGAGTGATTTCATTACACTCATAGTAGTATAAAAAGAGATACATTTCCC  
 TCTTAGGCCCTGGGAGAGAGACGCTTAGATTTCCCTACTGGCAAGGTTTAAAAATGAGGTAAATGCCGTAT  
 ATGATCAATTACCTTAAITGGCCAGAAAATGCTTCAGGTGCTAGGGGTATCCCTGCAACACTGCAAGAACAA  
 AGGTCAATAAGATCTTGCCATGAATACCCCTCCCTTTTGCGCTGTAAATTTGCAATGAGAAGCAAAITTACA  
 GTACCAATACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCAATAAACTGTGATTAAAGAAATCTA  
 CCTCTCGTATGGCTGTTACTGTACTGTACTCTGACTCTCACTAACAATGAATTTGTTACATAACTCTCT  
 ACATGTATGATTTTGTGCCACTGATCTTAAACCTATGATTCAGTAACTTCTTACCATATAAAACGATAATTTGCTT  
 TATTTGGAAGAAATTTAGGAATACTAAGGACAATTTTATAGACAAGTAAAAAGACAGATATTTAAGAGG  
 CATAACCAAAAAAGCAAACTGTAAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACGTGTTTATCTGCTT  
 CATATGCTTTTAAITTTTCAATTTCAATTTCAATTTCAAAATAAGATTTAGTAAAGCTGTTTATCACTT  
 AACAGCTCAITTTGTCTTTTCAATATACAAATTTAAAAATACCTACAAATTTTAACTAAGGCCAACCCGATTTC  
 CATAAATGTAGCAGTTACCGGTCTCACTCACATAAGGCTTAGAGTTGCTGTGATGCAITTTGATGATTAAT  
 GTATGCTGTTCTTCTCATGTAATGTCAAGACATGGAGGTTGTTGTAATTTTATGTGAAATTAATCCTCTTAA  
 CACATATTTGCTTAAAAATGTCAAAAAATGAGCACTTACAATGTATGCTCTCAATGAAGATTTCTTAT  
 GTGAAATTTAAAGACATGATTTCGCGATGAAGGATTTTCACTGGAAGTACAATAAGCACAATCAGGTGTTG  
 CTCAACTGCTTTATCACTATAAACAGCCATCTTAAATAGCAACGATTTGTGAGTACTGATGTATATAATAA  
 AAATTAACAAGGAAA

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## **FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196  
><subunit 1 of 1, 229 aa, 1 stop  
><MW: 26017, pI: 4.73, NX(S/T): 0  
MGDKIWLPPFPVLLLAALPPVLLPGAAGFTPSLDSDFTFITLPAGQKECFYQPMPLKASLEIEY  
QVLGDGAGLDIDFHLASPEGKTLVFEQKSDGVHTVETEVGDYMFCCFNTFTSTISEKVIFEL  
ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDRN  
IQESNFDRVNFWSMVNLVVMVVSAIQVYMLKSLFEDKRKSRT

### **Important features:**

#### **Signal peptide:**

amino acids 1-23

#### **Transmembrane domain:**

amino acids 195-217

#### **N-myristoylation site.**

amino acids 43-48

#### **Tyrosine kinase phosphorylation site.**

amino acids 55-62

105101-26187660

## FIGURE 182

CCATCCCTGAGATCTTTTTATAAAAAAACCAGTCTTTGCTGACCAGACAAAGCATACCAGAT  
CTCACCAGAGAGTTCGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCTCGGATG  
CTGCTTTTCCTGCCTCATTCTCCTGTGTGAGGTTCAAGGTGAAGAAACCAGAAGGAAGTCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTCACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTGCTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGACGCTCATCATGGACATGAGACCAGTGTGAAGAT  
TCACCCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTATGATCCTCC  
TTCCTTTTCCCTTTTCTTACCTTCATTTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

0978192-101501

## **FIGURE 183**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM

DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIWGLHDPDPTQGSEPDGDGWEWSS

TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPHYVCKFKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

09978192.101501



## FIGURE 184

CCAGTCTGTGCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGTGGC  
TGCTTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGA CTCCACGGTGACCAAGTCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCTGCCCGTGTCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGCCCTCACGCTC  
CTCCCACTCTTGAGCCTCCGACTGTAGAGTCCCCGCCACCCCATGGCCCTATGCGGCCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

0997819.101501

## FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVGIGQTLFVSCCNTELCNVDGAPALNSLHCGALTLLPLLSRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

09978192.101501

## FIGURE 186

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCTGACTCTGCAGCCGAACCGGC  
ACGGTTTTCTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTTTCTTTCTCCCTCTT  
GAGTCTTCTGAGATGATGGCTCTGGGCGCAGCGGAGCTACCCGGGTCTTTGTGCGATGG  
TAGCGGCGGCTCTCGGCGGCCACCTCTGCTGGGAGTGAGCGCCACCTTGAACTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAAATGGAATATGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGAGA  
GACACTAAACCAGCTATCCAAATGCAGTGAACTCCTTTTATATAATAGATGCTATGAAAACC  
TTTATGACCTTCATCAACTCAATCCTAAGGATATACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACCTCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTCTAAAGGTGCTGCACTGCCTATTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAGCATAACCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGAATGACAAATGATAGGTACCTAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

09978192.101501

## FIGURE 187

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTIIDNYQFYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRKRRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKRRRGKSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSRLHTCQRH

**Important features:**

**Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

09370392.101501

## FIGURE 188

TGTGTTTCCCTGCAGTCAGAAATTTGGGACNGCAGGGGTTCCCGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTCTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCACCGNTGGGCGGCGCTGCGGGGCACCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

09978192.101501

# FIGURE 189

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCGCGGTGTCGCTGCACCTCACCAATCCCGTGCGCCGCGG  
 CTGGGCGCTCGGAGAGTGCCTGTGCTCTCTCTGTCAGCGGTGCTTGGGCTCGGCCAGGCGGGCTCCGCGGCCA  
 GGGTTTGGAGATGGGGGAGTAGCTACAGGAAGCGACCCCGGATGGCAAGGTATATTTTGTGGAAATGAAAAGSA  
 AGTATTAGAAATGAGCTGGAAGCCATTACAGATTAATATTTTGGGGACAGATTTGTGATGCTTGATTCCACCT  
 TGAAGTAAGTAGAGACAGAGTCTCAAAATTTGCATATTACATCAACTGGAACAGCAGAGTGAATCTTAAATTTACTTC  
 TTAATACAGACATCTGCATAAGAAAGAGAAATGGGAGTCTGGTTAAATTAAGATGACTATATCAGAGATCTGAAAG  
 GATCAITCTCTGTTTTCTGATATGTGTATATGGCCATTTTGTAGGCGACAGATGAGTATTTTACAGTTTACTTTGG  
 AGTGTCACAACTGCAAGCAGTAGAGAAATAAGACAGCTTTCAGAGAAATGGCATTTGAAGTTACATCTCTGATAA  
 AAAACCCGAATAACCCAAATGCAATGGCGGATTTTAAAAATAAATAGAGCATATGAGTACTCAAGATGAAGA  
 CTCTACGGAATAAGATGACAAATATGGAGAAAGGGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
 CTATTATCGTTATGATTTTGTGATTTTATGATGATGATCTGAAATCATAACTTGGAAAGAGAATTTTGTATGC  
 TGCTGTTAAATTTCTGGAGAACTGTGGTTTGTAAATTTTACTCCCCAGGCTGTTCACACTGCCATGATTTAGCTCC  
 CACATGGAGAGACTTTGCTAAAGAGATGGATGGGTTACTTCGAATTTGGAGCTGTTAACTGTGGTGATGATAGAAT  
 GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCAGCTCTCTTCATTTTCGGTCTGGAATGGCCCGAGTGAATA  
 TCTATGGAGACAGATCAAGAGGAGATTTAGTGAGTTTTCGAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
 CTCAGGAAATTTTGTCAACTCCATACAACTGCTTTTGTGCTGGTATTTGGCTGGCTGATCACTTTTGTTCAAA  
 AGGAGGAGATTTGTTGACTTTCACAGACAGCTCAGGCTTTAGTGGCATGTTGTTCCTCAACTCATTTTGTTCAGTAA  
 AGAAATATATTTGGAAGTAATACATAATCTTCAGATTTTGAATCTACTTCGGCAACACAGTACAGAGATCGTTT  
 GGCTCCTACTCGGTGGCTGTATTTTTCATTTTGGAAAAAATGAAATTTCAATGATCTCGAGCTGAAAAAAT  
 AAAAATCTACTTAAATGATCATATTCAAGTTGGCAGGTTTGAATGTTCTCGCACAGCATCTGTGATGAAA  
 TCTGTATGTTTTCAGCGCTCTCAGCAGTATTAAAGACGAAGATGGAATGATGAAATTCATCATGGAATA  
 GAAGATCTCATATGATATACTTGCCCTTTGCCAAAGAAAGTGTGAATTTCTCATGTTTCCACGCTTGAGCTCAAAA  
 TTTTCTGTCCAATGACAAAGAACATGGCTTGTGTGATTTCTTTGCCCTGTGGTTCAGCAGCTGACGAGCTTTACT  
 ACCAGAGTTACAGAGAGCATCAATCTCTTTATGTCAGCTTAAAGTTTGGTACACAGATGATGACAGTTTCATGA  
 GGGACTCTGTAAACATGTATAACATTCAGGCTTATCCAAACAGCTGATTTCAACAGCTCAACATTCATGAGTA  
 TGAAGGACATCACTCTGCTGCAGCAAACTCTGGAGTTTCATAGAGGATCTTATGAATCCTTCAGTGTCTCCCTTAC  
 ACCCACCACCTTCAACGACCTAGTATTCACAAAGAAAAACACACGAAGTCTGGATGGTGTATTTCTATCTCCCTG  
 GTGCTCATCTTGGCAAGCTTAAATGCCAGAAATGAAAAAGATGGCCCGGACATTTAACTGAGATCAATGAGAAAT  
 CTGGGGTCTAGGAATTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTTCAGTGAAGAAAGTTCTACAGG  
 GAAAAATCATTTGGGTGATTGATTTCTATGCTCTTGGTGTGGACTTGGCCAGAATTTTGTCCAGAATTTTGAGCT  
 CTGTGGCTAGGATGATTAAGGAAAAAGTGAAGGCTGGAAAAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA  
 AGCTGGGATCAGGGCTATCCAATCTGTTAAGTTTATTTTCTACGAAGAGACAAAGAGAAATTTTCAAGAAAGACA  
 GATAAATACCAGAGATGCAAAAGCAATCGCTGCCCTAATAAGTGAAGAAATTTGGAAGCTTCCGCAAGATCAAGGCAA  
 GAGGAATAAGTGAATCTTGAATGTTGAAGATGAAGAAAAAGTTTAAAGAGAAATCTCAGACATGACATCAG  
 AAGACACCTATTAGAAATGTTACATTTATGATGGGAATGAATGAACATTTATCTTAGACTGTGAGTTGTACTGCCA  
 GAATTATCTACAGCACTGGTGTAAAGAAAGGGTCTGCAAACTTTTCTGTAAAGGGCCGGTTTATAAATATTTTGA  
 GACTTTGAGGCTTATAATATATGTTTTCACATGAGAAACAGAAATAGAGTCATCATGATTTCTTTGTTATTTGCT  
 TTTTAAACACTTTTAAAAAATATTAAGACGATTTTACTCAGAGCCATGAAAGTAGGCTGGATTCAGTCCAGT  
 GACCATAGATGCTGCTCCCTCGACGGAATTTATAATGTTTCAAGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
 ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCTCCTCAGTTTTTTGGCTGAGCTGAAAAAGGGTAACT  
 TAGTTTGTGGTCACTGTTCTCTCAAAATGCTATCCCTAACCATATTTTATATTTCTGTTTAAAAAACCCCAT  
 GATGTCAGCTGAACAAACCCCTGTTATGCTGTATTAATATGAGGAGATTTCTCATTTGTTTCTTCTCTCTCA  
 AAGGTTTGAAGAAATGCTTTTAAATTTTTCACAGCCGAGAAACAGTGCAGCAGTATATGTCACACAGTAAGTACAC  
 AAATTTGAGCAACAGTAAGTGCAGCAAAATCTGTAGTTTGTGTATCATCCAGGAAACCTGAGGGAACAAATTA  
 TAGCATTAATCGGGCATGTAGAGATATCCTAAATATGTTATCAAGTATTAGAGTTCTTATTTTAAAGATATA  
 TGTGTTCAATGATTTTCTGAATTTGCTTTCATAGAAATTTTCCACTGATTTGATTTTGTAGGCACTTAATAT  
 TTACATATTTGCTCTGCACTTTGTTTGTGACCTGTATCTCTTATTTACATTTGGGTTTCTTCTCATGTTTGGT  
 TTTTCTACTCTGTCAGCTCTATTTATTTTCAATAGGAAAAATCTTTACAGGTTGTTTCTGATGAGCTTAT  
 AATGATAGCTGATGTTTCTCCAGTTACTAGTTTACTGTGACAGGGCTGCTTTTTCAGATAAATATGACATATA  
 ACTGAAGTTATTTTATAAGAAATCAAGTATATAATCTTAGGAAAGGATCTTTCAGTTCTGTGTTTGTAGA  
 CTCAGAGATCACAATTTTGTGAGTAACTGTAGTTGTTTGTATTAATTTACAGAGTGTACAGATGGTAAAAAT  
 CCAATCAGTCAAGAGGGTCAATGAATTAAGAGGCTTGCACCTTTTCAAAAAA

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## FIGURE 190

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSSLGVSKTASSREIRQAFKKLALKL  
HPDKNPNPNNAHGDFLKNINRAYEVLKDEDLRKKYDKYGEKLEDNQGGQYESWNYYRYDFGI  
YDDDDPEIITLERREFDAAVNSGELWVFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFIFRSGMAPVKYHGDRSKESSLVSFAMQHVRSVTTELWTGNFVNS  
IQTAFAAGIGWLITFCCKGGCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLDPDFELLSAN  
TLEDRLAHHRWLLFFHFGKNENSNDPELKKLTKLLKNDHIQVGRFDCSSAPDICSNLVVFQP  
SLAVFKQGQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYQQLKFGTLDCTVHEGLCNMYNIQAYPTTVFNQSNIEHEYEGHHS  
AEQILEFIEDLMNPSVSVSLTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYS LRIWGLG  
FLPQVSTDLTPQTTFSEKVLQGNHWWIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC  
QAYACTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGRNKDEL

### **Important features:**

#### **Endoplasmic reticulum targeting sequence.**

amino acids 744-747

#### **Cytochrome c family heme-binding site signature.**

amino acids 158-163

#### **Nt-dnaJ domain signature.**

amino acids 77-96

#### **N-glycosylation site.**

amino acids 484-487

09978192-101501

## FIGURE 191

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGG  
GTCGTTGGTGAAAGTTTTTTCATTCTCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TTACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGTTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTGGATCACAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTTACAGAGGTCTGCATCAGAACTTCAGGCCTT  
GGGAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCCACA  
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTGTCCATCGTATATCAATATCTTTCTGAG  
ACTACAGAAGTTTCTTCTCTGAACGCGCTCAGCGATTTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATGCAATAAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTGAATCAATGCTGCAAAGCTTTATTTACATTTTT  
TCAGTCTGTATAATATTA AAAACATTGGTTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCTGTTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGCTGTTTTTCTCTT  
TCATGCCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTTATTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGAAGGTTTAAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAAGATTGAGCATTTGAAAGATTTCCCTAGCCCTCTTCTTTT  
TCATTAGCCCAAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAAGTGGACCCTCTATATTTCTCTCCCTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAAGTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTTCATATATCTCTGGTCCCAGAGATGTTTAGACAAAT  
TTTAGGCTCAAAAATTAAAGCTTAACAAGGAAAGGAACTGTACTGGCTATTACATAAGAAA  
CAATGGACCCCAAGAGAAGAA

0979192-101501



## FIGURE 192

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAACRKLGVTAHAYVVDCSNREEIYRSLNQVKEVGDTVIVVNNAGTV  
YPADLLSTKDEEITKTFEVNI LGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGVFHRGLTSELQALGKTGIKTSCLCPVFNVTGFTKNPSTRLWPVLETDEVVRLID  
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

### **Important features:**

#### **Signal peptide:**

amino acids 1-19

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

#### **Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

00978132 101501

## FIGURE 193

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGCCCGGAGAGGGCCAGCCGCGCCGGGGC  
AGGATGACCAAGGCCCGGCTGTTCGGCTGTGGCTGGTGCTGGGGTCGGTGTTCATGATCCT  
GCTGATCATCGTGTA CTGGACAGCGCAGGCGCGCGCACTTCTACTTGACACGTCCTTCT  
CTAGGCCGCACACGGGGCCGCCGCTGCCACGCCCGGGCCGACAGGGACAGGGAGCTCAGG  
GCCGACTCCGATGTGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAAGGAGACGGAGCAGCGCGCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCGCGCAGCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCA ACTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCAAGGTGGCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGACACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCGCTACGGGAAGCTCT  
CCCCCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCTCTTCTGTCGCGGACCCC  
TTCGTGCGCTGATCTCCGCTTCCCGCAGCAAGTTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCGGTGCCCATGCTGCGGCTGTACGCCAACACACAGCCTGCCCGCTCGCGCG  
GCGAGGCCTTCCGCGTGCGCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAATCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACTCTCTCC  
GAGACTTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCCCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTAAGATTAATATATTTTCAGGTATTTAATACGA

## FIGURE 194

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSMILLIIIVYWDSAGAAHFYLHTSFSPHTGPPLPTPGPDRDELTA  
DSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFFPTKERAFDDIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLS  
GSLLHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELENEEFYRKFAVPMRLRYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

### **Important features:**

#### **Signal peptide:**

amino acids 1-31

#### **N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

#### **TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

09978192-101501

## FIGURE 195

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCCAGAGTAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTTCGTGACCGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCGGGC  
CCTGGAGCAGGAGCTCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTGTCAACAAC  
GCTGGCCACCACCCACCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGAATGTTCATCAACATCTCCAGCCTGGTGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCAG  
CCTAGGGCCGCATGGGCCAGCCCGCTGAGGTGCGGGCTGCGGCAGTGTTCCTGGCCTCCGA  
AGCCAACTTCTGCACGGGCATTGAACCTGCTCGTGACGGGGGTGCGAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCGTGGACGCCCCGATATCCCTTCCTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCCTAGGACTCTCCACCCCAAACCTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCAGTTAGCAAGGTGCCGGGTACCCCTGCAGGTTCCCAT  
AAAAACGATTTCAGCC

0976192.101501

## FIGURE 196

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVVTGGGRGIGAGIVRAFN SGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLCDVNVNAGHHPPQRPETSAQGFRLLELNLGTYTLTKL  
ALPYLRKSQGNVINISLVGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAAVFLASEANFCTGIELLVTTGG  
AELGYGCKASRSTPVDAPDIPS

**Important features:**

**N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

09978192.101501

## **FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGACAGCTTGGCGGAATGACTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCATCTTCTGGGGCTGGGCCAGCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGGCCCTCACCAGGTGCCACTGGACC  
TGGTGTCACGGATGAAACCGTATGCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCAGCTGAGGAACAGCTCAGAGCTGGCCAGAGAAAGTGTGAGGTCAACTGCGAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTCAGCCAGGTTCTGTGCGCCGCCG  
CCTCTGCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCAGAAAGCCAGGCCAGCAGCCCGAGA  
CCATCCTCCTTGACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

09978192.101501

## **FIGURE 198**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKQGGRPGPLAPGPHQVPLDLVSRMKFYARMEFY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPISRIPVDLPEARCLCL  
GCVNPFITMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIavgctCIF

**Important features:**

**Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

0973192.107501  
105707.262460

## FIGURE 199

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGGCCGGCCGCTGCGCTTCCCCACACTCCCGCCGAGAAAGCCTCGCTCG  
GCGCCCAACATGGCGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCGTGGAT  
CGCGGGCTGTGGCGGCGACGGCAGGCCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCGCGG  
TCCAGCCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT  
TACGCCCCCATGGTGTCCATCCTGCGCAGCAGACTGATTCAGAAATGGGAGGCTTTTGCAGAGAA  
TGGTGAAATATCTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCCAGGTTTGAAGTG  
GCCGCTCTTTTGTACCACCTCTCCAGCATTTTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGGCCCCAGGAATCTTGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACTATTTCACAGTGACTCTTGGAAATT  
CCTGCTTGGTGTTCTTATGTGTTTTTCGTCTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAAAAGACAGCCCTGTAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACTTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCTGCCCCAGC  
TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAGTCAGCATGCTGACAAGGGAC  
TGTAGATTAAATGATGCGTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAATCCTTAATTTTTCTGAAATGAGCAAGCTTCTCTTAAAGATGCT  
CTCTAGTCATTTTGGTCTCATGGCAGTAAGCCTCATGTATATAAGGAGAGCTTCCAGGTGT  
GACAATCAGGATATAGAAAAACAAACGTAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTTAGGGGTGAGAGAGTCTCGACAGAGGAGGCCATTCCAGTCTCAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAATGAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAGTGTAACGTAGAAGCCTTGCATCCTTTCTTGTGTAAAGTATTAT  
TTTTGTCAAATTGCAAGAAACATCAGGCACCAAGTGATGATGAAAAATCTTTCACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTACCTTTAATTTTTCCAGCATTTCCACCATGGGCATTGAGGCTCT  
CCACTCTTCACTATTATCTCTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATGTTTTGTCCAAATATAGTTGTTGTTGATTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCTCTAAGTCTTGGCAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACGTGTTTTGTTTTCATCTCAAGGGGTTCCCTGGGTCTTGAAC  
TACTTTAATAATACTAAAAAACCACTTCTGATTTTCTTCTCAGTGATGTGCTTTTGGTGAAC  
GAATTAATGAACTCCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC  
TTCCAAAGAAATATATCTTTGTAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

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## FIGURE 200

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSCQQTDSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFFRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLQDEDEAEEEEEEEDNLAAGVDEERSEANDQGPPGEDGVTRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSKHADKGL

### **Important features:**

#### **Signal peptide:**

amino acids 1-22

#### **Transmembrane domain:**

amino acids 191-211

#### **N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

#### **Flavodoxin proteins**

amino acids 173-187

0978192.101501

**09**

ATCTGGTTGAAGTACTACTTAAGCTTAATTGTTTAAACTCCGGTAAGTACCTAGCCCCACATGAGTT  
TGACTCAGAGATTCTCTTTTGCCACAGCAGTCATCTCAGGGGCGAAGAAAGAGAGCTCC  
CAAAATGCTATATCTATTACAGGGGCTCTCAAGAA~~CAAT~~TGGAATATATCTGTAATTTAGAAAAAT  
TTGGATAGAGATGGATATCTCAATTACACTTCGACTCTCAAGACCAATACCAGGATAGCTGT  
TGTTTTCAGAGAAAGGATCTGTGTCGCATCTCTCTCTGGCGCCTCATTTGCTTAATTTTGG  
GAATCCTATGCTTTGGTAATATCTGGTAGAGTCTGGTCTCTGGGTACCATGGGGGTTCTTTC  
AGCCCTTGTCTCTTAATTGGATTATATATGAGAAGAGCTGTATCATATTTCAGCATGTGCATCT  
AAATCTCTGGATGGAAGTAAAGAACAATGCTGGCAACTGGGCTCTAATCTCTTAAGATAAT  
ACAGCTCAAAATGAATTTGGGATTTATAGTAAAAACAAGTGTCTTCCCAACCTGATAATTCTATT  
TGGATAGGCCCTTTCTCGGCCACAGCTGAGGTACAGTACCTGGCTCTGGGAGGATGGATCAACATCT  
CTCTCTTAACCTATTTCAGATCAGAACCAAGCTACCCAGA~~AAAA~~CCGATCTCCAAATTTGTG  
TATGGATTACGTGTCAGTCAATTATGACCAACTGTGTAGTTGTGCCCTCATATAGTATTGTT  
GAGAAGAAGTTTTCATGT~~TAG~~AGGAAGAGGGTGGAAGAGGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAAACAGAACAGAAAAAGGTAACAGCTGAGGTCAAGATAAATGCAGAAAAATG  
TTTAGAGAGCTTGGCCCAACTGTAACTCTAACCAAGA~~AAAT~~TGAAGGAGAGAGGCTCTGTATTTCT  
GTATTTGTGCACTCAGAGTAGGCTAGTATTAATTTTCTAGTTAGTAGATCTGTAGACATGG  
AATCAGGGCAGCCCAAGCTTGAAGTTTATTTTATTTTATTTATTTTATTTTGTGATAGGGTCT  
CACTTTGTTACCAGGGCTGGAGTGCAGTGGCGACAATCTGCATCACTGCTCAGCATCTCTCTGC  
CTCAGCCCTCAAGTAGCTGGGACTGAGTGCAGTGCATGCCACTGCAGGCTAAATTTTGGTG  
TTTTTTGTAGAGACTGGGTTTGGCCATGTTGACCAAGCTGTGTCTCTAATCTCTGGGCTTAA  
TGATCTGCCCCCTCTGGCCCTCCCAAGTGCTGGGAGTACAGATCTGGAGCCACACCTGGC  
CCCAAGCTTGAATTTCTATTCTGCCATTGACTTGGCATTTACTCTGGGTAAAGCCATAAGCGA  
ATCTTAATTTCTGGCTCTCATCAGATGTGTTTCTATGCTCAACATGCCATTTGAAGTGCACGGT  
GTGTTGCCAGGATTTGACCCCTCAACTCTACAGCATATCAGTTATGAATCTGAGGGTGAAT  
ATATTTCTGAATAGCTAAATGAAAGAANTGGGAAAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTATTTCTCATGATATGATCATAAATTTATGATTATCATCTTAGTAAAAAGCAGGAATCTCTA  
CTTTTCTTTTACATTAATAAATAGCTCAGAGAGTACATCTGCATCATCTCTAATGAATCTTT  
TTTTTTTCTTTTCTTTTGTAGACAGAGTCTTTCGCTCTTGTGTGCCCAGGCTCGGAGTGCAACGG  
CAGCATCTCGGCTCACCGCACTCGGCCCTCGGGTTCAAGCAATTTCTCTGCTCAGCCT  
CCCAAGTAGCTGGGATTAAGTACAGTCAGGCACACCAACACCGGCTAAATTTTGTATTTTGTAGT  
AGAGACAGGGGTTTCTCATGTGGTCAAGGTAGTGC~~CGCA~~ATCTGCATCTCAAGTGAATCTGCT  
CTGCTCTGGGCTCCCAAGTCTGGGATTAAGGCTGAGGCATCGACCCAGCCTAGAATCT  
TGTATAATATGTAATTTGAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTAAATACA  
AAAAATACATAAAATACATAAAATCTGATGATGAATATAAAAGATTAACCACTCATTTGGA  
ACAAGTATTACATTTTGGAAATGTTTATTATGTTTGTGATGACTGTTTTCATTTTACAATTTT  
ACCAATTTTTTTCAGTAATTACTGTA~~AAAT~~GTGATTATGGAATGAACATATATTTCTCATG  
TGCTGATTTGTCTATTTTTCATATTTTCCACTGGTGTCTTTTATTTTCCAATGGATA  
TTTCTGATTACTTAGGAGGCTTTACAGTCTCTAATGTTGATTAATATGTGAAAAGAAAT  
TGTACCAATTTTACTAAATATGCAAGTTTAAATGGATGATTTTATGTTATGTTGGAATTTTCAT  
TTCATTA~~AAAA~~AAAAATCTTATCA~~AAAA~~AAAA~~AAAA~~AAAA~~AAAA~~AAAA~~AAAA~~AAAA~~AAAA~~AAAA~~AAAA~~AAAA

## FIGURE 202

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912  
<subunit 1 of 1, 201 aa, 1 stop  
<MW: 22563, pI: 4.87, NX(S/T): 1  
MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGS CAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFSMSLNSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

### **Important features:**

#### **Type II transmembrane domain:**

amino acids 45-65

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

#### **N-myristoylation sites.**

amino acids 35-40 and 151-156

#### **Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

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# FIGURE 203

GGAGGGGAGGAGCAGGCCACACAGGSCACAGGCCGGTGAGGGACCTGCCAGACTGGAGGGTCTCGCTCTGTCA  
CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCGGCTTCAAGTGATCTCATGCC  
TCAGCTCTCCGAGTCTGGGATTCAGGTGGTGACTTCACAGGTGACTCCGTGGAGGAAAATGATCTCCCCAG  
TGCTGCTGCAGACGACATCTTCTGCTGAGTCTGCTCTTCTGGTCCAGGTGCCACAGGCGAGGGCCACAGG  
GAAGACTTTTGGCTTCTGAGCCAGCGGAACACAGACACAGGAGCAGCTCCACTACAACCCACACAGCACTG  
CGATCTCCATCCAGAACTCCGAAGAGGGCCCTCAGAGTCCATGCCCTTTCCCTGCAGGCCACCTTGCTTCCGA  
TCCTTCCCTGACCCAGGGGGCTTACCATTCTGCGCTCTATGGAACCGAGATCTGGGAGGATTAATCTTTCT  
TATGGCAAGCGTGACTTTCTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCAGCACACAGGAGGAGGCTG  
GCTCAGGGCCCCCGCTGTGTAGCCACTTCTGTCACTCCTGGTGGAGCCTCAGAACATCAGGCTGCCAGTGGCC  
GCCAGCTTCACTTTCTCTTCCACAGTCTCTCCACACAGGCCGCTCACAATGCTCTGGTGGACATGTGCGAGCTC  
AAAGGGACCTCCAGCTGCTCAGCCAGTTCTGAAGCATCCOCAGAAGGCTTCAAGGAGGCCCTCGCTGCCCTC  
GCCAGCCAGCAGTTCAGAGCCTGGAGTGGAACTGACCTCTGTGAGATTCAATGGGGGACATGGTGTCTTCAG  
GAGGACCGGATCAACGCCACGGTGTGAAGCTCAGGCCACAGCCGGCTCCAGGACCTGCACATCCACTCCCGG  
CAGGAGGAGGAGCAGAGCAGATCATGGAGTACTCGTGCTGCTGCTCGAACATCTTTCAGAGGACGAAGGCG  
CGGAGCGGGGAGGCTGAGAAGAGACTCTCTCTGGTGGACTTCAGCAGCCAGGCGCTGTTCAGGAACAAGATTC  
AGCCAAAGTCTGGGTGAGAAGTCTTGGGGATTGTGTACAGAACACCAAGTAGGCCAATCTCAGGAGCCCGGT  
GTGCTCACTTTCCAGCACAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTTGAAGACCCACA  
TTGAGCTGAGCCCGGGGAGTTCGAGAGCTGTCGGGTGTGAGACCGTCAGGAGAGAACCACAACTCTGCTTCTG  
AACCATCAGCCACTACTTTGAGTGCTGATGGTCTCTCTGGTGGAGGTGGAGCGCGTGGACAGCCTGTGCTGAGC  
CTCTCTCTCTAGCTGGGCTGTGTGCTCTCTGCGCTGGCCTGCTTGTCAACATGCGCGCTACTCTGTCTCCAG  
GTGCCCTCGCGTCAGAGAGGAACTCGGAGTACACCATCAAGGTSCATGAACTGTGCTGCTGCGCGCTTCTC  
CTGCTCGACACAGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGG  
ATCTTCTGCTCACTCTCCCTGCTCATCTGCGCTTCTGGATGGGCTCAGGGGGTACAACTTACCAAGCTCGT  
GTGGAGGTCTTTGGCACTTCTCCCTGGCTACTACTCAAGCTGAGCGCATGGGCTGGGGCTTCCCATCTTT  
GGGTGAGCTCAGGCTGCCATGTGCTGGATCCGGAGTCCCTGGTCACTACATCACCACCTGGGCTCTTCAGC  
CTGGTGTCTTCTGTTCACTATGACCATGCTAGCCACCATGCTGGTGGAGATCTCCGCTGGCGCTTTCACCT  
AAGTGTTCACATGTGCTAGCAGCTGCTGGGCTCAGCGTGTCTTGGCTGGCGCTGGGCTTGTATCTTCTCTCC  
TTTGCTTCTGGCACTTCCAGCTTGTGCTCTTCACTTTTCAGCATCATCACTCTCTTCCAGGCTTCTCATC  
TTCATCTGATCTGTTCCATGCGGCTCAGGCCCGGGGTGGCCCTCCCTCTGAGAGGCACTCAGACAGCGCC  
AGGCTCCCCATCAGCTCGGGCAGCACCTGCTCAGCCGCTATCTAGGCTCCAGCCACCTGCCATGTGATGAAG  
CAGAGATGCGGCTCGTGCACACTGCTGTGGCCCCGAGCCAGGCCCGAGCCCCAGGCCAGTCCAGCGCAGAT  
TTGGAAGCCCCACGACCATGAGAGATGGGCGGTGCCATGTGTGGAGCGACTCCCGGGCTGGGCTTTGAATTG  
GCCTTGGGGACTACTCGGCTCTCATCAGCTCCACCGGACTCAGAAGTGCOCGCGCATGTGCTGCTAGGGAATG  
TCCCCACATCTGTCCCAACCCAGCTGGAGGCTGTGCTCTCTTACACCCCTGGGCCCCAGCCCTCATTTGCTGGG  
GGCCAGGCTTGGATCTTGAGGGTCTGGCACATCTTAATCCTGTGCCCCCTGGGCGGGAAGAATGTGGCTCCA  
GTGTCTCTGCTCTCTGTGTCACTCAGGCGCACTCTGCTCTCTGTCAATTTAACTCAGGTGGCACCCAGG  
CGAATGGGGCCCCAGGCCAGACCTTCAAGGCCAGAGCCTGGCGAGGAGAGGCCCTTTCAGAGGACACAGCAGC  
AGCTCGGCTACTCTGAGCGAGGCCCTCCCTCCCTCAGCCCCCAGTCTCCCTCCATCTCTCTGGGGTTC  
TCCTCTCTCCGCCGGGCTCTTCTCTCTCTGTTACAGCTGGGGGTCCCGATCCCAATGCTGTTTTTGGGGA  
GTGGTTTCCAGGAGCTGCTGTGTCTGTGCTGAATGTTTGTCTACTGCACAAGCCTCGGCTGCCCTGAGCCA  
GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCTCTGTCCATCTGGGCTTTGTATGAGCTGCATTGGCCCTTG  
CTCACTCTGACCAAGCACAGCCTCAGAGGGGCCCTCAGCCTCTCTGAGGCCCTCTGTGGCAAGAACTGTGGA  
CCATGGCCAGTCCCGTCTGGTTTCATCCACCTCAAGGACTGAGACTGACCTCTCTGTGTGACACTGGCCTA  
GAGCTGAGCTACTCTCTAAGAGGTTCTTCCAGGCCCCCAATAGCTCCAGGCGCCCTCGGCGGCCCATCATGT  
TAATTTCTGCAACAAACACACAGCGGTAGATTGTCTGCTGTTGTAGTGTAGGGAACAGATGACAGCAGCTG  
GTCACTCTCTCTGCAACATTCAGTGTGTATGTGAGGCGTGGTGAAGCAAGAACTCTCGAGCTACAGGACA  
GGGAGGACATCTGCTGCTGGGAATCTGGAAGACTTCTGAGGAGTCTGCTGAGGAGTCTGTCACTTGAAGAT  
GGGAAGGATGTTCTTTTACGTACCAATTTTGTCTTTTGATATTAAGGAAGTACATGTTCAATGTAGAGA  
ATTTTGAATCTGAGAGAGATCAGAGAAATAAAAAATCACTGTGTGAATCAGTACCAAAAAA  
AAAAA

09978196.101501

## **FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSQLQTTLFLLSLFLVQGAHGRGHREDFRFCSQRNQTHRSSLHYKPTPDLRISIENSE  
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASFTTFSFHSPHTAAHNASVDMCELKRDQLL  
SQFLKHPQKASRRPSAAPASQQLQSLESKLTSVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTLFTQTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTEPVVLTFOHQLOPKNVTLQCVFVVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMMVSSVEVDVAHKHYLSLLSYVGCVVSAACLVTTIAAYLCSRVLPC  
RRKPRDYTIKVHMMNLLAVFLDTSFLLSEPVALTGSEAGCRASAIFLHFSLLTCLSWMGL  
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLVSYITNLGLFSLVFLFNMAMLATMVVQILRLRPHTQKWSHVLTLGLSLVLG  
LPWALIFFSFSAGTFQLVVLVLFISIITSFQGFLIFIWYSMRLQARGGPSPLKNSDSARLP  
ISSGSTSSSRI

### **Important features:**

#### **Signal peptide:**

amino acids 1-25

#### **Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

#### **Microbodies C-terminal targeting signal.**

amino acids 691-693

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

#### **N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

#### **G-protein coupled receptors family 2 proteins**

amino acids 475-504

09978192-101501

## **FIGURE 205**

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTG CAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACCTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACCTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGCCT  
GGTGTTTCTGTTCAACATGG

0978192-101501

# FIGURE 206

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGTTTCAGGTCAGGTTTTCGCTTTGA  
 TCCTTTTCAAACCTCGAGACACAGAAAGGGCTCTAGGAAAAAGTTTGGATGGATATATGTGAAACACCTACCT  
 GCGATTCTCTGCTGCGACAGGAGCGCTCGGCGCTTCCACCCCGTGCAGCGCTTCCCTGGGCGTGGTGAAGAGAC  
 TCGGGAGTGTGCTCTTCAAAGTGCCTCGGCGGCTGAGTGAGCTCTCACCCAGTCAGCCAAATAGCGCTCTTCGGGC  
 TTCTCGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGCGGAACTCAACCTGAGTAGTAATTCG  
 AGTTTTCCAGCAACAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTTACTGTGTCTACTAATG  
 GAAGTATTCACAGCCCAAGGTTTCTCATACTTATCCAAGAAATACGGCTCTGGGTATGGAGATTAGTAGCAGTAG  
 AGGAAAAATGTATGGATACAACCTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGGAAGATGACATATGCAAGT  
 ATGATTTTGTAGAAAGTTGAGGAACCCAGTGATGGAACATATATAGGGCGCTGGTGTGGTTCTGGTACTGTACAG  
 GAAAAACGATTCTAAAGGAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTCTGAACACGGGT  
 TCTGCATCCACTACAACATTGTCTATGCCACAATTACAGAAGCTGTGAGTCCCTCAGTGCTACCCCTTCAGCTT  
 TGGCACTGGACCTGCTTAATAATGCTATAACTGCCCTTAGTACCTTGAAGACCTTATTCGATATCTTGAACAG  
 AGAGATGGCAGTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTGTTTTTGGAA  
 GAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACCTCGTAACCTCT  
 CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG  
 GTGGGAACCTGTGCTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
 ACGAGGCTCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGC  
 ACCATGAGGAGTGTGATGTGTGTGACAGGGGAGCACAGGAGGATAGCCGCAATCACACAGCAGCTCTGGCCA  
 CAGCTGTGCAGTGCAGTGGCTGATTTCTATAGAGAAGCTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGGCT  
 TCAAGGACCTTTTCATCTTCAGGATTTTACAGTGCAATCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCA  
 ACAGCTCTTTTGGAGAGGAGCGCTAAAGGACAGGAGAAAAGGCTCTCAATCGTGGAAAGAAAATTAAGTTGTGAT  
 TAAATAGATCCACAGCTAGTTTTCAGAGTTACCATGTACGTATTCACCTAGCTGGGTTCTGTATTTTCAGTTCTTTT  
 GATTAAGCTTACGGTCTAGGCTGTGATTCAGTACAGGAAAAAACTGTGCAAGTGAACCTGATTCGGTGTGCTTTAAC  
 TCTAAAGCTCCATGTCTCTGGGCTAAAAATCGTATAAAATCTGGATTTTCTTTTCTTTTCTTTTCTGCTCATATTCACAT  
 ATGTAAGCCAGAACATCTATGTACTACAAACCTGGTTTTTAAAGGAACATATGTTGCTATGAATTAACCTGT  
 GTCATGCTGTATAGGACAGCTGGATTTTTCATATTTCTTATTAATAATTTCTGCCATTGAGAAGAGCAACTACA  
 TTCATGGTTTGAAGAGATAAAACCTGAAAGAGAGAGTGGCCTTATCTTCACTTATCGATAAGTCAGTTTATTTG  
 TTTCAATTGTGACATTTTATATTTCTCTTTTTCAGATTATACTGTTGGGCTTTTCTAATCTTTGTAAATATATCT  
 ATTTTACCAAAGGATATTAATATTTCTTTTTATGACAACTTAGATCAACTATTTTGTAGCTTGGTAAATTTTTCT  
 AAACAAATTTGTTATAGCCAGAGGACAAAGATGATATAAAATATTTGTCTGTGACAAAAATACATGTATTTCA  
 TTCTCGTATGTGCTCAGAGTTAGATTAATCTGCATTTTAAAAACCTGAATGGAAATAGAAATGGTAAGTTGCAAA  
 GACTTTTGAATAATTAATATATCATATCTTCCATTCTGTATTGGAGATGAAATAAAAGCAACTTATGA  
 AAGTAGACATTAGATCCAGCCATTACTAACCTATTCTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACAT  
 AAAGCACCTGAAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTGTGCTGTGAGTAGGAACACATCTCTATT  
 TTGTGATGTTGTGGTTTATATCTTAACTCTGTCCATACACTTGTATAAATACATGGAAATTTTTATGTACA  
 GAGTATGTCTCTTAACCACTTCACTTATTGTACTCTGGCAATTTAAAGAAAAATCAGTAAATATTTTGTCTGT  
 AAAATGCTTAATATNGTGCTAGGTTATGTGTGACTATTGAATCAAAATGATTTGAATCATCAATTAAGAA  
 ATGTGGCTATTTTGGGAGAAAAATTAATAAAAAAAAAAAAAAAAAAGGTTTAGGATACACAGGTTATGCGGCC

09978192.101501

## FIGURE 207

MSLFGLLLLSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWIIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPKGQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPSPALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGKRSRVVDLNLLEEVRLY  
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ  
LRPKTGVRGLHKS LTDVALEHHEECDCVCRGSTGG

**Signal sequence:**

amino acids 1-14

09978192-101501



# FIGURE 208

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTCTCTTCAACCAGACCTCTACATTCCATTTTGGGAAGA  
 AGACTAAAAATGGTGTTCCTCAATGTGGGACACTGAAGAGACAAATCTTATTCCTTTTAAACNTAATCTTAAATTTCCAA  
 AAACCTCTTGGGGCTAGATGGTTTCTTAAACCTCTGCCCCCTGTGATGTCTACTCTGATGTCTTCAAAGAACCAATCTGTG  
 ATCTGTGGACTGCACAGACAGCAATTTGACAGAAATCTCTGGAGGTATTTCCCAAGAACACACGAACTCTCACCTCTC  
 ACCATTAAACCACTACACAGACTCTCCCCAGCGTCCCTTTCACAGACTGGACACTCTGGTAGAGATCGATTTTCAGA  
 TGCACCTGTGATCTATTCCACTGGGGTCAAAAACACACATGTGCATCAGAGAGCTGTGAGATTAAACCCAGGAAGC  
 TTTAGTGGACTCACTTATTAAAAATCCCTTTTAACTGGATGGAAACACAGTACTAGAGATACCGCAGGGCTCTCCCG  
 CCTAGCTTACAGCTTCTCAGCCTTGGAGGCCAACACATCTTTTCCATCAGAAAAGAGAAATCTTAAACAGAACTGGCC  
 AACATAGAAATATCTTACCTGGGCCAAAACCTGTTATTATCGAAATCCTTTGTTATGTTTCATATTCAATAGAGAAA  
 GATGCTCTTCTAAACTTGAACAAAGTTAAAGTGTCTCCCTGAAAGATAACAATGTACAGAGCCGCTCCCTACTGTT  
 TTGCCATCTACTTTTAAACAGAACTATATCTTACACACAACTGATTGCAAAAATCCAAGAAGATGATTTTAAATAAC  
 CTCACCAATATACAAATCTTTCAGCTTAAGTGGAAATGCCCCGTTGTTTATAATGCCCAATTTCCTTGTGCGCGCG  
 TGTAAAAATAATTTCTCCCTACAGATCCCTGTAAATGCTTTTGTATGCGCTGACAGAAATTTAAAGTTTTCAGTCTA  
 CACAGTAATCTCTTTCAGCATGTGCCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACGGATCTGTCC  
 CAAAACCTCTTGGCCAAAAGAAATGGGGATGCTAAATTTCTGCAATTTCTCCCGAGCTCATCCAATTTGGATCTG  
 TCTTTCAATTTTGAACCTCAGGTCTATCTGTGCATCTATGAATCTATCACAAAGCATTTTCTTCTACGAAAAGCCGTG  
 AAAATTTCTGGGGATCAGAGGATATGTTCTTAAAGAGTTGAAAAGCTTTAACTCTGCGCATTCATATAATCTTCAA  
 AATCTTGAAGTTCTTGTATCTTGGCATAACTTTATAAAAATTTGCTAACCTCAGCATGTTTAAACRAATTTAAAGAA  
 CTGAAAGTCATAGATCTTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAGTGAAGTTGGCTTCTGCTCAAAAT  
 GCCAGAACTCTCTAGAAAGTTATGAACCCCAAGTCTCTGGAACAAATACATATTTCAGATATGATAAGTATGCA  
 AGGAGTTGCAGATTCAAAAACAAAAGAGGCTTCTTTTCATGCTCTGTTAAATGAAAGCTGTGACAAGTATGGGCAGACC  
 TTTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGTCTCTGATTTTCAGCATCTTTCTTCTCTCAATGCCGTG  
 AATCTGTGAGGAATCTCATTTAGCCAACTCTTAATGGCAGTGAATTTCCAACTTTAGCAGAGCTGAGATATTTTG  
 GACTTCTCCAACACCGGCTGATTTTACTCCATTCAACAGCATTTTGAAGAGCTTCAACAACTGGAAGTTCTTGGAT  
 ATAAAGCAGTAAAGCCATTAATTTTCAATCAGAAGGAATTTACTCATGTCTTAACTTTTACCAAGAACTTAAAGGTT  
 CTGCGAAGATCTAGATGAACGACAACTGACATCTCTTCTCTCACAGCAGGAGCTGAGAGGTGAGTCTCTTAGA  
 ACTCTGGAATTCAGAGAAATCACTTAGATGTTTATGGAGGAAGGTTGATACAGATCTTCAATCTTCAAG  
 AATCTGCTTAAATTTAGAGGAATTTAGACATCTCTAAAATTTCCCTAAGTTTCTTGGCTTCTGGAAGTTTGTATGGT  
 ATGCTCTCAAATCTTAAAGAACTCTCTTTGGCCAAAATGGGCTCAAATCTTCAGTGTGAGAAACCTCCAGTGT  
 CTAAGAACTCTGGAATCTTTGGACCTCAGCCACAACTGACCACTGTGCCCTGAGAGATTATCCAATCTGTCC  
 AGAAGCTCAAGAACTTGATCTTTAAGAAATCAATCAAATCAGGAGTCTGACGAATATTCTTCAGAGATGCGCTTC  
 CAGTTGCGATATCTGATCTCAGCTCAAATAAAATCAGATGATCAAAAACCCAGCTTTCCCAAGAAATGTCTTC  
 AACAACTGAGAGATGTGCTTTTGCTATCAATATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGG  
 GTTAAACCATACGAGGTGACTATTCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAGGGGC  
 CAAAGTGTGATCTCCCTGGATCTGACACTGTGAGTTAGATCTGACTAACCTGATCTGTTCTCACCTTCCATA  
 TCTGTATCTCTCTTTCTCATGGTGTATGACAGCAAGTCACCTCTATTCTTGGGATGTGGGTATATTACCAT  
 TTTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTGCTATGATGCTTTTATTTGTGTAT  
 GACACTAAAGACCAGCTGTGACCGAGTGGGTTTGGCTGAGCTGTTGGCCAACTGGAAGACCCCAAGAGAGAAA  
 CATTTTAAATTTATGCTCGAGGAAGAGGACTGGTTTACAGGGCAGCCAGTCTTGGAAAACCTTTCCAGAGACATA  
 CAGCTTAGCAAAAAGACAGTGTGTTGTATGACAGACAAAGTATGCAAAAGACTGAAAATTTTAAAGATAGCATTTTAC  
 TTGTCCCATCAGAGGCTCATGGATGAAAAGTTGATGTATTTCTGTGATATTTCTGGAAGGCCCTTTCAAGAG  
 TCCAGTCTCTCAGCTCCGGAAGAGGCTCTGTGGAGTTCTGCTGAGTGGGCCAACAAACCCGCAAGCTCAC  
 CCGATCTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAACTCATGTGGCTCTATGTCAGGTGTCTCAAGGAA  
 ACGGTCTAGCCCTCTTTTGCAAAACCACTGCTAGTTTACCAAGGAGAGCTGGC

09978192.101501

## FIGURE 209

MVFPMWTLKRQILILFNIIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG  
IPTNTNTNLTLTINHIPDISPASFHRDLHVEIDFRCNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLEIIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYR  
NPCYVSYSIEKDAFLNLTCLKVLSLKDNNTAVPTVLPSTLTLEYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPPCAPCKNNSPLQIPVNAFDALTELKVLRHNSNLQHVPWRWF  
KNINKLQELDLSONFLAKEIGDAKFLHFLPSLIQLDLFSNFELQVYRASMNLSQAFSSLSKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDTGTFNIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYQG  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVQLKMMNDNDISSSTSRMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL  
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSCLKNLILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMILLHHNRFLCTDAVWFVWVWNHTEVTIP  
YLATDVTCVGPGAHKQSVISLDLYTCELDLTNLILFSLSISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPATTEWVLAELVAKLEDPREKHFNLCLEE  
RDWLPQGQPVLENLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIIILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHPHYFWQCLKNALATDNHVAYSQVFKETV

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

0978192.701501

# FIGURE 210

GGGTACCATTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGACACACAGAAACATGGAAAAACATGTTCCCTTC  
 AGTCGTCAATGCTGACCTGACATTTTCCTGCTAATATCTGGTTCCTGTGAGTTATGCGCCGAGAAAAATTTTCTTA  
 GAAGCTATCCTTGCTGATGAGAAAAAGCAAATGAGCTCAGTTATTGTCAGAGTGCAGCAATCTGCTGACATACGGAAG  
 TTTCCCAAACGCTGGGCAAAATATGTGACAGAACTAGACCTGCTGTGATTAATTTTCATCACACACATAACGAATGAAT  
 CATTCTCAAGGGCTGCAAAATCTCATATAAAATAAATCTAAACCCAACTGATGACAGCAGACAGAACGGAAATC  
 CCGGTATACAATCAATGGCTGGAATATCACAGACGGGGCAATCTCTCAACCTAAAAAACTTAAGCGGAGTTATCTGC  
 TTGAAGACACACAGATTCCGCCAAATACCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTTAATTCAAAAACA  
 ATATATAACAACATACTAAGAGAGGGCATTTCAAGACTTATAAACTTGAAAAATCTCTATTGGCTGGAACTGTCT  
 ATTTTAAACAAAGTTTGTGCGAGAAAACTTAACATAGAAGATGGAGTATTGAAACGCTGACAAATTTGGAGTTGCTCAT  
 CACTATCTTTCAATTCTCTTTTCAACGCTGCCACCCAAATCTGCAAGCTCCCTACGCAAACTTTTTCTGAGCACA  
 CCGAGATCAATATCTTGTAGGAAGAGTTTCAAGGGATTGATAAATTTAACTATAGATTAAAGCGGAACT  
 GTCCGAGGTGCTTCAATGCCCATTTTCCATGCGTGCTTGTGATGGTGGTGCTTCAATTAATATAGATCGTTTGTG  
 CTTTTCAAAACCTTGACCCAACTTCGATACCTAAACCTCTAGCACTCCCTCAGGAAGATTAAATGCTGCTGGT  
 TTAAAAATATGCTCATCTGAAGGTGCTGGATCTTGAATCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT  
 TTTTAACGATGCTGCCCGCTTAGAAATCTTGACTTGTCTTTAACTATATAAAGGGGAGTTATCCACAGCATA  
 TTAATATTTCCAGAAACTCTCTAAACTTTTGCTCTACGGGCATTGCAATTAAGAGGTTATGTGTTCCAGGAAC  
 TCAGGAAGATGATTTCCAGCCGCTGTAGTGCAGCTTCAAACCTATCGACTATCAACTGGGTATTAATTTTATTA  
 AGCAAACTGAATTTCAAACTTTTCCAAATTTTCCAAATCTGGAATTTATTTCTGTGACAAAAACGAATATCAC  
 CTCTGGTAAAGATATCCCGGCAGAGTTATGCAAAATAGTTCTCTTTCAAGCTCATCTCGAAACAGACGCTCAA  
 CAGATTTTGAAGTTTGACCCACATTCGAACCTTTTATCATTTTCAACCCGCTCTTAAATAAGGCCAAATGTGCTGCT  
 ATGGAAAGCTCTTAGATTAGCGCTCAACGATATTTTCTCATTTGGGCCAAACCAATTTCAATGAACTTCTGCTGACA  
 TTGCTCGTGTAAATCTGTCTGCAAAATAGCAATGCTCAAGTGTAAAGTGAACGAATTTTCAAGCCATCTCTAGT  
 TCAAATATTTGGATTGACAAAACAATAGACTAGACTTTGATTAATGCTAGTGCTCTTACTGAAATCTGCAATTTTAA  
 AAGTTCTAGATCTAGCTATATAATTTCACTAATTTCAGAATAGCAGGCGTAACACATCAATAGAAATTTATCAAA  
 AATTTCAACAATCTAAAGTTTAAACTTGAGCCACACAAACATTTATATCTTAAACAGATAAGTATACCTGTGAAA  
 GCAAGTCCCTGGTAGAATTTAGTTTCTAGTGGCAATCGCTTGACATTTTGTGGCAATGATGACACACAGGTATATA  
 TCTCCATTTTCAAGAGTCTCAAGAATCTGACACGCTGGGATTTATCCCTTAATAGGCTGAAGCACTCCCAAGT  
 AAGCATTTCTTAATTTGCCAGCGCTCTCACTGAACATACATATAAATGATAATGTTAAAGTTTCTTAACTGGA  
 CATTTACTCCAGCAGTTTCTCTGCTCGAGTTGCTTGACTTACGTGAAACCAAACTCATCTTTTAACTGATAGCC  
 TATCTGACTTTTACATCTCCCTTCGGACACTGCTGCTGAGCTATAACAGGATTTCCACACTCCCTCTGGCTTTCT  
 TTTCTGAAGTCAGTAGTCTGAAGCACTCGAATTAAGTTTCAATCTGCTAAAAACCAATCAACAAATCCCGCACTTG  
 AAACTAAGACCACCAACCAATTTATCTATGTTGGAACTACACGGAAACCCCTTTGAATGCACTGTGACATTTGAG  
 ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTCACAGACTGGTAGATGTCAATTTGTGCCACTCTG  
 GGGATCAAAAGAGGGAAGATATTGTGAGTCTGAGGCTAACAACTGTGTGTTTCAGATGTCACTGCAAGTGAATTA  
 TTTTCTTCACTGTTCTTTTATCACCACCATGGTTATGTTGGCTGCTGGCTCAACATTTGTTTATCTGGGATGTTT  
 GGTTTATATAATGTGTGTTTAGCTAAAGTAAAGGCTACAGGCTCTTTTCCACATCCCAAACTTCTATGATG  
 CTTACATTTCTTATGACACCAAAGATGCTCTGTTACTGACTGGGTGATAAATGAGCTGCGCTACACCTTTGAAG  
 AGAGCCGAGACAAAAAAGCTTCTCTTTGCTAGAGGAGAGGGATTGGGACCCGGGATGGCCATCATCGACAAC  
 TCATGACAGCATCAACCAAAGTCAAGAAAAAGTATTTGTTTAAACAAAAAATATGCAAAAGCTGGAACTTTA  
 AAACAGCTTTTACTTTGGCTTTGACAGGCTAATGGAATGAGAACTGGATGTATATTATTTCTCTGAGGAC  
 CAGTGTACAGCATCTCAGTATTTTGGAGGTACGGCAGCGGATCTGTAAGAGCTCCATCTCCAGTGGCCCTGACA  
 ACCCGAAGGCGAGAGGCTGTTTGTGGCAAACTCTGAGAAATGTGGTCTTCTGACAAATGATTACGCGTATAACA  
 ATATGATGTGCTATCCATTAAGCAATCTAACTGACGTTAAGTCATGATTTTCCGCCATTAATAAGATGCAAG  
 GAATGATCATTTCTGATATTAGTTATGTTGCTATGTACAAATATCCAAAACTTAGTGCTTTTAAAAACAG  
 TTGCTGGGCCCAAGTTTGTGGGGTTCAGGAGTCCAGGCCACGACATACTGGGTCTCTGCTCAGGTTGCTCTGAG  
 AGGTGCTCATGTAGGTTTCTCACCAGACATAGGCATCTGGGTGCTGAGTGTGTTTCTTGTGATTTCA  
 ATTTCTCTCTGGGCTATTTGGCCAAAGCTATCTCATGTAAAGCCATCGAGGCTCTCCCAACAGGCGAGTGTCTTC  
 ATCAGAGCTAGCAAAAAAGAGAGGTGCTGACGAAGATGAGTCAAACTTTTGTGAATGCAATCAAAAGAGTGAT  
 ATCTCATCACTTTGGCCATATTCTATTGTTAGAAAGTAAACCAAGGCTCCCAAGCTCCATGGAGGTGACCC  
 CTAGTCCAGGAAAAACAGCTGAAGCAAGATGCTGAGCTCTGATTTGCTGAGTCACTCAATCTATTTCCT  
 TGACTGCTGCTCTGGGATGGCTGCTATCTGATGATAGATTGTGAATATCAGGAGCCAGGATCTAGTGTGAGC  
 ATCTTAGCAGTGTGACCTAACACATCTCTTTTCAATATCTAAGAACTTTTGGCACTGTGACTAATGGTCTTAATA  
 TTGCTGTGTTGTTTATATTATCATATCTATGGCTACATGGTTATATGCTGTGGTGGCTTGGTCTGGTCTTAT  
 TTACAGTGTGCTTTTACAAATATTGCTGTAACTTTGACTCTTAAGGTTTATAGATGCCATTTAAGAACTGAGATG  
 ATAGCTTTTAAAGCATCTTTTACTCTTACCATTTTTAAAAAGTATCAGACTAAATTCGAGGATTTTGGTCTATA  
 TTGTTAATTGCCATTGCTGTAATCTTAAAAATGAATGAATAAAATGTTTCATTTTACAAAAAAGAAAAA

09978192.101501

## FIGURE 211

MENMFLOQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPTVG  
KYVTELDLSDNFIITHITNESFQGLQNLTKINLHNPNVQHONGNPGIQSNGLNITDGAFNLN  
KNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEEDFKGLINL  
TLDDLSGNCPCRCFNAPFCVPCDGGASINIDRFAPQNLTLQLRYNLNLSSTSLRKINAAWFKNM  
PHLEKVLDELFNYLVGEIVSGAFLTMLPRLEILDLSFNLIKGSYPQHINISRNFSKLLSLRAL  
HLRGYVFQELREDDFQPLMQPLNLSLSTINLGINFIKQIDFKLFQNFNSLEIYYLSENRI SPLV  
KDRQSYANSSSFQRRHIRKRRSTDFFEFDPHSNFYHFTRLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELS DLEV  
LDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLTDKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTE LHINDNMLKFFNWT  
LLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTL LLSHNRI SHLP SGFLSEVSSLKHL DLS  
SNLLKTINKSALETKTTTKLSMLELHG NPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFF TFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQTIFYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWD PGLAID  
NLMQSINQSKTVFVLTKKYAKSWNFKTAFYLA LQRLMDENMDV IIFILLEPVLQHSQYLRL  
RQRICKSSILQWPDNPKAEGLFWQTLRNVVLTENDSRYNMYVDSIKQY

### **Signal sequence:**

amino acids 1-26

### **Transmembrane domain:**

amino acids 826-848

0978152.101504

## FIGURE 212

CCAGGTCCAAC TGCACCTCGGTTCTATCGATTGAATTC CCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCCGTGCCGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGTTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCTCTCA  
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCTGCCAGGCCTCGCTACGCGTGTGCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCTTGGGGCTGTGGAGCAGCAATATGCCAGCCGCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGTGCCGCTGCCCTGCAGGATGGCGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGTCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCCTGTGTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCGACAGGAGTGGACAGTGAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGTGGAGGAGAAGCTGCAGCTGGTGTGGC  
CCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACTCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTCTCTTCTCTG  
GAGGAGCAGCTGGGGTCTGTCTCTGCAAGAAAGACTCGTGA CTGCCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTACGCCGCCCTGCAGCCCCATGCCCTGCCCCAACATGTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCC  
TCTCTCGGGAGGCTCCCCAGACCCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCTTGCTACCCCCAACGGCATCCCAAGGCCAGGTGGGCCCCCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCAGAGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCTCAGTGGGGCTGTGCTGACCCCCAGCACAAATAAAATGAACGTGA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

0976192.103501

## FIGURE 213

MRGSQEVLLMWLLVLA VGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL CVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

Signal sequence:

1-19

09978492.101501

## FIGURE 214

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCTGTGGTTGGCAGCAAAGTTCAGCTTGGCTGGGCCGCTGTGA  
GGGCTTCGCGCTACGCCCCTGCGGTGTCCCGAGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGCCCCGGGAGGGGAACCTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGTGTATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGTGTGTCCGGGCTCACGGGGACCTGTCTCCGAGTCGTTCTG  
TGCAGCGTGTGTACAGGCCCTTCTCACCACTGCGACGGGCACCGGGCCTGCAGACCTAC  
CGAACCATCTATAGGACCGCTACCGCCGAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCTTGGGGCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGTAGGAGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTGGGAGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCAGGGTGGCCCCAACCCG  
ACAGGAGTGGACAGTGCATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGTGCGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGCAGCCTCCTGGTGCACCTCTCCAGCAGCTCGGCCGATCGAC  
TCCCTGAGCGAGCAGATTTCTCTTCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA  
CTCGTGACTGCCCCAGCGCTCCAGGCTGGACTGAGCCCTCACGCCGCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCTTCCTCCTCCCCCTCCTCGGGAGGGCTCCCAGACCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCTGGCTACCCCCACCTGGCTACCCCCAAGGCA  
TCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCTCAGTGGGGGCTGCTGCCTGAC  
CCCCAGCACAAATAAAATGAAACGTG

05976192-101501

## FIGURE 215

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSDGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKDS

**Signal sequence:**

1-19

0978192.101501



## FIGURE 216

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGC  
AGTGGGCGGCACAGAGCACGCCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACG  
GGGACCTGTCTCCGAGTCGTTCTGTGCAGCGTGTGTACCAGCCCTTCTCCACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAAACCATCTATAGGACCGCCTACCGCCGAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGTAGGAGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGTTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGAGCCTCCTGGTGCCTCC  
TTCAGCAGCTCGGCCGATCGACTCCCTGAGCGAGCAGATTTCTTCTGGAGGAGCAGCT  
GGGGTCTGTCTCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCTCTCTTCTCTCTCCCTTCTCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCTGGCTACCCCAACGGCATCCCAAGGCCAGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGTGAGCCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGG  
CCTCAGTGGGGGCTGTGCCTGACCCCGCAGCAATAAAAAATGAAACGTG

0978192.101501

## FIGURE 217

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRCVAVRAHGDPVSESFVQRVYQPFLTTCGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRRCR  
CPAGWRGDTCCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLADGTL CVPKGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSSEQISFLEEQLGSCSCKDS

Signal sequence:

1-19

09978192.101501

# FIGURE 218

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGTCAGGAGGAGACAGCCTCCCGCCCCGGGGAG  
 GACAAGTGCCTGCCACCTTTGGCTGCCAGCTGATTCCTTGGGACGGTCCGCTTCTCGCGCTCAGCTGCCGGCCG  
 AGTTGGGTCTCGGTGTTTCAGGCCGGCTCCCCCTTCTGGTCTCCCTTCTCCGCTGGGGCCGGTTTATCGGAGG  
 AGATTGCTCTTCAGGGCTAGCAATTGGACCTTTTGATGATGTTTGAACCCAGCGCGAGGAATAGCAGGCAACGTGAT  
 TTCAAAGCTGGGGCTCAGCCTCTGTTTCTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATTCGAATCA  
TGCTGTGATGGTGTGAGAAAGAGGTGACACGGAAATGGGAGAAACTCCAGGCAGGAACACCTTTTGCTGTG  
 ATGGCCGGCTCATGATGGCCCGGCAAAAGGGCATTTTCTACTGACCTTTTCTCATCTGGGGACATGTACAC  
 TCTTCTTGCCTTTGAGTGCCGCTACCTGGCTGTTCAGCTGTCTCCTGCCATCCCTGTATTGTGTCATGCTCT  
 TCCTTTTCTCCATGGCTACACTGTTGAGGACCACTTCAGTGACCTGGAGTGATTCCTCGGGGCTACCAAGATG  
 AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGGGTGCCCGAGGGCCAGCGACCAACGCCCTCGTA  
 TCAAGAATTTCCAGATAAAACAACAGATTGTGAACTGAAATACGTGTACACATGCAAGATCTTCGGGCTCCCC  
 GGGCTTCCATTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG  
 TTGAAAGAGGAACTACCGCTACTTCTACTCTTCATCTTTTCTCTTCCTCTCACAATCTATGTCTTCGCT  
 TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAATTTGGCTTCTTGGAGACATTGAAAGAAACTCCTGGAACGT  
 TTTAGAACTCTCATTGCTCTTTTACACTCTGGTCCGTGTGGGACTGACTGGATTTCATACCTTCTCTGTGG  
 CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAAATCGGCTCCAGAAATCCCTACAGCC  
 ATGGCAATATTGTGAAGAACTGCTGTGAAGTCTGTGTGGCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA  
 TTTTGGCACTGGAGAAAGTGAAGTCACTCCAGTACTCAAGAGACCAAGTAGCAGCTCTTGGCCACAGAGCC  
 CAGCCCCACAGAACCACTGAACTCAAATGAGATGCCGAGGACAGCAGCACTCCCGAAGAGATGCCACTCCAG  
 AGCCCCACAGCCACCAAGGAGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTT  
 TAATTAGGGCTATGAGAGATTTCAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTGAAGCTGCTCTTTAACT  
 GTTTTTCTTTGGTCTTTAGTGACCCAGTTGCACTCGGCAITTTCTGTGCAAGCTTTTAAATTTCTGAAT  
 CAAAGCAGTGGCAGAAGATGTCAGTCACTCTGATAACTGGAAAAATGGGTCTCTTGGGGCCCTGGCCTGTTCT  
 CCATGGCTCAGCCACAGGGTCCCTTGGACCCCTCTCTTCCCTCAGATCCAGGCCCTCTGCTTGGGGTCA  
 TGGTCTCATTTCTGGGCTAAAGATTTTTGAAGTGGCTCAAACTCTCCCAAGCTGCTGCAGCTGTGAGTCCAGA  
 GGCAGTCAAGAGACCTCTGGCCAGGGGATCTTAACCTGGGTCTTGGGGTCTTTCAGGACTGAAGAGGGGAGAG  
 TGGGGTCAAGAAATCTCTGGCCACCAAGTGCCAGCATTGGCCACAAATCTTTTAGGAATGGGACAGGTACCT  
 TCCACTTGTGTANNNNNNNNNNNNNNNNNNNNNNNTTGTTTTCTTTTGACTCTGCTGCCATTAGGAG  
 CAGGAATGGCAGTAATAAAAGTCTGCATTTTGGTCACTTTCTTCTCAGAGGAAGCCGAGTGTCACTTAAAC  
 ACTATCCCCCAGACTCCCTGTGTGAGGCCCTGACAGAGGCCCTGAATGCAAAATGGGAAACCAAGGCAAGAGAG  
 GCTCTCTCTCTCTCTCTCTCCCCGATGTAACCTCAAAAAAAGAAATGCTAACCAAGTTCTTCCATTAGGCT  
 CGGCTGAGTGAGGGAAGCCAGCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCCCTGGGCCACCTCTGGCT  
 ATGGTAACCACTGGGGCTTCTTCCAGCCCGCTCTTTCAGCACTTCCACCGGACAGTCCCAGAGCCACTT  
 CACCTGCGGGGTGGGTGTGGCCCCCAGTCAGCTCTGCTCAGGACTGCTCTATTTCAGGGAAGAAGATTTATGT  
 ATTATATGTGGCTATATTTCTTCAAGCACTGTGTTTCTCTCTTCTTAAAGCCAGGGTCTGCTGAGTACTTAT  
 GCGGTGGGGGATGTAAACCGGAATCTTTCACTTATTGAAGGCAATTAACCTGTGCTAATCA

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## **FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTLFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKYCYTCKIFRPPRASHCSICDNCVERFDHHC PWVGN CVGKRNYRYFYL  
FILSLSLLTIIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLCFFTLWSVVGLTGPHTF  
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVL CGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEPEDSSTPEEMPPPEPPPEPPQEA AEAEK

### **Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

09978192.101501

## FIGURE 220

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCITTTCT  
CCCACAGAGCNCCTTCGACCATCACTGCCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCNCCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT

09978192.101501

## FIGURE 221

GTGTGTCTCTCAGCAAAACAGTGGATTAAATCTCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAGAAAAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATATT  
GACAACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTGTAGAGATTT  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTACCGTGAACATATCCACCATACA  
TTTCAGAAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAAACAGACCTTCTCTCAAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGAACTACACTTTCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGCGCGCGTCAGCGAGGTGAGCAACGGCAGCTCGAGGAGGGCAGG  
CTGCGTCTGGCTGTGCTCTTCTGGTCTTGACCTGCTTCTCAAATTTTGAATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCACCAACACACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGACAGA  
AATTTGAGGGAGGGGAACAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAAACGGGAAGAACACAGC  
ACACCCGCTTGGACCACTGCAAGCTGCATCGTGCAACCTCTTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCCAGCTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACCTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAA

097019.101501

## FIGURE 222

MKTIQPKMHNSISWAIFTGLAALCLFQGVFVRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVVLLSNTQTQYSIEIQNVVDVYDEGPYTCVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYECASNDVAAPVVRVKVTNYPPIYISEAKGTGVPVGQKGTLCCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGNITCVASNKLGHNTNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVHLHLLKF

**Signal peptide:**

amino acids 1-28

09978192.101501

## FIGURE 223

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

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# FIGURE 224

ATGGCTGGTGACGGCGGGGCCGGGACGGGGCCGGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
 ATCACCGCCTGGGCCGACTCTCACCA**ATGA**ACGTCGCGCTCGAGGAGCTGGGAGCTGGGCAGCAACGTGGGATTCAG  
 AAGGGGACAAGACAGCTGTTAGGCTCAGCACGCACTGGAGCTGGTCTTAGCAGGTGCTCTCTACTGCTGGCT  
 GCACCTGCTCTCGGGCTGCTCTGTGGCCCTAGGGGTCAGTACACAGAGACCCATCCACAGCACTGCTCTTAC  
 GAGGCTCGCATTCGAGTGGCTGGAAAAATCTGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC  
 CAGTTCTCTGTGGGGGCTGGATTTCGAGGGAACCCCTGCCGATGGCGTCTCTGCTGGAAACCTTCAACAGC  
 CTCTGGGACCAAAACAGGCCATACTGAAGCACTGCTTGA AAAACCACTTCAACTCCAGCAGTGAAGCTGAG  
 CAGAAGACACAGCGCTTCTACTATCTTGCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA  
 GACCTCATTTGAGAAGATTGGTGGTTGGAAACATTACGGGGCCCTGGGACAGGACAACCTTTATGGAGGTGTTGAAG  
 GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCACCGCTCTACATCAGTCCGCACTCTAAGAGTTCCAACAGC  
 AATGTTATCCAGGTGGACCACTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAAGTCCCAATGAG  
 AAAGTGCTCACTGCTCTATCTGGATTACATGGAGAACTGGGAGTGTCTGGGTGGGGCCCACTCTCCAGAGG  
 GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAAACATCACAGTGGCCCAAGGACAGCGCGCGAC  
 GAGGAGAAGATCTACCAAGATGAGCATTTCTGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTGAGTTT  
 CTGTCTTTCTTGCTGTCAACATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTATGGGATGGATTATTTGCAG  
 CAGGTGTGAGAGCTCATCAACCGCAGGGAACCAAGCATCTGAACAATTACCTGATCTGGAACCTGGTGAAAAG  
 ACAACCTCAAGCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGTGGAGACCCCTATGGCACTAAGAAG  
 TCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACAAGGATGAGCGCCCTGGCTTTGGCTTTGGGGTCACTCTTC  
 GTGAAGGCCACCTTTGACCGCAAGCAAGAAATTGACAGGGGATGATCAGCGAATCCGGACCGCAATTGAG  
 GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCCGAGGCGAGCCAAAGGAGAAGCAGATGCCATCTAT  
 GATATGATTGGTTTCCAGACTTTATCTGGAGCCCAAGAGCTGGATGATGTTTATGCGGTGACCAAGTTCCT  
 GAAGATTCTTCTTCCAAACATGTTGAATTTGTACAACTCTCTGCGCAAGGTTATGGCTGACCACTCCGCAAG  
 CCTCCAGCGGAGACCAAGTGGAGCATGACCCCGCAGACAGTGAATGCTTACTTCCAACTAAGATGAGATC  
 GTCTTCCCGCGTGGCATCTCTGACGGCCCTCTTATGCGCAACCAACGCGCTGATGACAAAGAGGAACTC  
 GGTGTGGTCAATGGGCGATGAGTTGACGCATGCTTTGATGACCAAGGGCGAGTATGACAAAGAGGAACTC  
 CGGCCCTGGTGGCAGAAAGTCCCTGGCAGCCTTCCGGAACCAACGCGCTGATGAGGAGAACAGTACAATCAA  
 TACCAGGTCAATGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAAACATTACTGACAAAGCGGGGCTGAAG  
 GCTGCTTCAATAGCTTTCAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCACTGCCAGCCGTGGGGCTCACC  
 AACCAAGCTCTCTCTGCTGGGATTGCCCCAGGTGTGGTGTCTGGTCCGACACACAGAGAGCTCTCACAGGGG  
 CTGGTGACCGACCCCAACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCAACTCCCGTGACTTCTGCGG  
 CACTTCCGCTGCCCTGTGGCTCCCCATGAACCCAGGGCAGCTGTGTAGGTTGTGGT**AGA**ACCTGGATCAGGGGA  
 GAAATGGCCAGCTGTACACAGACCTGGGGCAGCTCTCTGACAAAGCTGTTTGTCTTGGGTTGGGAGGAAGCAA  
 ATGCAAGCTGGGCTGGGCTAGTCCCTCCCCCAACAGGTGACATGAGTACAGACCTCTCTCAATCACCAATGG  
 TGCTCTGCTTTGGGGGTGCCCTGCCCTCAGCAGAGCCCCCACTTCACTGTGACATCTTTCCGTGTACCCCT  
 GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGATCTGCC

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## FIGURE 225

MNVALQELGAGSNVGFQKGTQQLGSRQTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA  
ILKHLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFPTVYIISADSKSSNSNVIQVDQSGFLFLPSRDYYLNRTANEKVLTA  
LDYMEELGMLLGGRPTSTREMQQVLELEIQLANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGMDYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLLLETLYGTTKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTAFFEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF  
FQNMNLNLYNFSKVMADQLRKPPSRDQWSMTPQTVNAYYLPKNEIVFPAGILQAPFFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAPFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPAVGLTNHQLFFVGFQAQVWCS  
VRTPESSHGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNPQGQLCEVW

**Type II Transmembrane domain:**

amino acids 32-57

0970192.101501

[illegible][illegible]

## FIGURE 227

GGCCGAGCGGGGGTGTCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCCGCGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC  
TCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCCTGCATTGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCACTTCTCCTGTGGGGGCTGGATTGGA  
GGAACCCCTTGCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAAACCACTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCATTCTTCAC  
CGTCTACATCAGTGCAGACTCTAAGAGTTC AACAGCAATGTTATCCAGGTGGACCACTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTACCTAGTGAACAACTGCCCT  
CCTTTCTTTCTTTCTTTCTTCTCCTCCCTCCCTCCCTTTCTTCCCTTTTCTTCTTCTTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCACTGTGATGGGTTTATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTGAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCTGAAGAGATTGCATTGAGCCAGGTCTGTAG

09978192-101504

## **FIGURE 228**

ATGCCTACTACCTTCCAAC TAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCC  
TTCTATGCCCCGCAACCACCCCAAGGCCCTGAAC TTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCC TTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAA TGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAG  
TACAATCAATACAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCGCTTCCGCGTGTGGGCACTCTCTCCAAC TCCCGTGACTTCTTGCGGC  
ACTTCGGCTGCCCTGTCTGGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGT CACCAGACCTGGGGCAGCTCTCTGACAAAGCTGT  
TTGCTCTTTGGGTTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCACA  
GGTGACATGAGTACAGACCCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTACCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCTGCCCCACTGTGACCCACAGGCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCACACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCCCTCAGGGCTACCCCACTCACCCGTGTCTCCTTGTGCCACTGCTCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCAATATGTGTAGCGGTACTGGTTCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAGGAAGAACAGAGTTTATTTTACAGAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

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# FIGURE 229

CCCACGCGTCCGAGCGCGCCGAGAATTAGACACACTCCGGAGCGCGCCAAAAGCAACCGAGA  
 GGAGGGGAGGCAAAAACACCGAAAAACAAAAAGAGAGAAACACCCCAACAACTGGGGTGG  
 GGGGAAGAAAGAAAGAAAGAAACCCACCCACCAAAAAAAGAAAAAAGAAAAA  
 AAAAAAAGAAATCCTGTGGCGCGCCGCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG  
 TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGATGGACATGATG  
 CTGTTGGTGCAGGGTGCTTTGTTGCTCGAACCACTGGCTGGCGGCGGTGCTCCTCAGCCTGTG  
 CTGCTGTCTACCTCTGCTGCTCCCGGCTGGACAGAGTGTGGACTTCCCTCGGGCGGCGGTGG  
 ACAACATGATGTGTCAGAAAGGGGACACGGCGGTGCTTAGGTGTTATTGGAAAGTGGAGCT  
 TCAAGGGTGGCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCAGT  
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAGGGACTACAGCCTCCAGATACAGAATG  
 TAGATGTGACAGATGATGGCCCATACAGTGTCTGTTCAGACTCAACATACACCCAGAACA  
 ATGCAAGTGCATCTAAGTGTGCAAGTTCCTCCTAAGATATATGACATCTCAATGATATGAC  
 CGTCAATGAAGGAACCAACGTCACCTTACTTGTGTTGGCCACTGGGAAACAGAGCCTTCCA  
 TTCTTGGCGACACATCTCCCATCAGCAAAACCAATTGAAATGGACAATATTTGGACATT  
 TATGGAATTAAGAGGACCAAGGCTGGGGAATATGAATGCACTGCGGAAATCTGTGTCAATT  
 CCCAGATGTGAGGAAAGTAAAGTTGTTGTCAACTTTGCTCCTCACTTTCAGGAAATTAAT  
 CTGGCACCCTGACCCCGGACGCGAGTGGCTGATAAGATGTGAAGGTGCAGGTGTGCCGCT  
 CCAGCCTTTGAATGGTACAAGGAGAGAGAAGCTCTTCAATGGCCCAACGAAGAAATTTATAT  
 TCAAAATTTTAGCACAAGATCCATTCTCACTGTTCACCAAGTGCAGCAGGAGCACTTCGGCA  
 ATTATACCTGTGTGGCTGCGCAACAGCTAGGCACAACCAATGCGAGCCTGCGCTCTTAACCT  
 CCAAGTACAGCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTCTCCTGCTGGTACCT  
 TGTGTTGACATGTCCTCTTTACCAGCATATTTCACTGGAAGATGCACTTCTCAATAAA  
 TTCAAGACCCATAAAGGCTTTTAAGGATCTCTGAAAGTGCTGATGGCTGGATCCAATCT  
 GGTACAGTTTGTTAAAGCAGCTGGGATATAATCAGCAGTGTCTCATGCGGATGATCGCT  
 TTCTGTAGAAATTGCTCATTATGTAATACCTTTAATTTCTACTCTTTTTTGATTAGCTACATTA  
 CCTGTGAAGCAGTACACATTGTCCTTTTTTAAGACGTGAAAGCTCTGAAATTTACTTTTAG  
 AGGATATTAATTGTGATTTTCATGTTTGTAACTCAAACTTTTCAAAAGCATTCAGTCATGGT  
 CTGCTAGGTTGCAAGCTGTAGTTTACAAAACGAATATTGCAAGTGAATATGTGATCTTTAA  
 GGCTGCAATACAAGCATTCAAGTTCCTGTGTTCAATAAGAGTCAATCCACATTTACAAGATG  
 CATTTTTTTCTTTTTTGATAAAAAAGCAATAATATTGCCCTTCAGATTTTCTTCAAAATA  
 TAACACATATCTAGATTTTCTGCTGTGATGATATTCAGGTTTCAGGAATGAGCCTTGTAAT  
 ATAACGGCTGTGCAAGCTCTGCTTCTCTTCTGTAAGTTCAGCATGGGTGTGCCCTTCATAC  
 AATAATATTTTTCTCTTTGTCTCCAATAATATAAAATGTTTTGCTAAATCTTACAATTTGA  
 AAGTAAAAATAAACAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAAACGAAGGAGC  
 TATTGGACTGTAAAAATCTCTCTGCACTGCAAAATGGGGTTTGAGAATTTTGCCCCACACT  
 AACTCAGTTCTGTGATGAGAGCAATTTAATAACAGTATAGTAAATATACCATATGATTTTC  
 TTTAGTTGTAGCTAAATGTAGATCCACCGTGGGAAATCAATCCCTTTTAAATGACAGCACA  
 GCCACTCAAAGGATTGCTAGCAATACAGCATCTTTCTTTCTAGTGTCCAAGCCAAAAA  
 TTTTAAGATGATTTGTGAGAAAGGGCACAAGTCTATCACCTAATATTACAAGAGTTGGTA  
 AGCGCTCATCAATTTTATTTTGTGGCAGGTATATGACAGTGCAGCCTGGAGGGTATGGA  
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACAGGGTGGTTATGACCGCTACTC  
 AGGAGGAAATACAGAGCAATTTATGACAACTGAAATGAGACATGCACATAATATAGATACA  
 CAAGGAATAATTTCTGATCAGGATCGTCTTCCAAATGGCTGTATTTATAAAGGTTTTTGG  
 AGCTGCACTGAAGCATCTTATTTATAGTATATCAACCTTTTGTTTTTTAATTTGACCTGCCA  
 AGGTAGCTGAAGCACTTTTAGACAGTTCATCTTTTTTTTTTAAATTTTTCTGCTCATTAA  
 AGACAAATTATGGCAGCTTTGTCAAAAAAAGAAAAAAGAAAAAAGAAAAA

## **FIGURE 230**

MMLLVQGACCSNQWLA AVL LSLCCLLP SCLPAGQSVDFPWA AVDNMMVRKGD TAVLR CYLED  
GASKGAWLNRSSI IFAGGDKWSV DPRVSISTLNKRDYSLQIQNV DVTDDG PYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEGTVTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFDPVRKVKV VNFAPT IQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQE HFGNYTCVAANKLGTNASLPL  
NPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLKNAILQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Transmembrane domain:**

amino acids 326-345

#### **N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

#### **Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

#### **Tyrosine kinase phosphorylation site.**

amino acids 178-186

#### **N-myristoylation sites.**

amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325

#### **Myelin P0 protein:**

amino acids 92-121

0976162.101501

## FIGURE 231

AGTGGTTGAGTGGGAAGGATCTTTCTCCAAGTGGTTTCCTTTGAGGGGAGCATTCTCTGCTGG  
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA  
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTACCAGAAATTGCAATGGAGCCTTTTGAAA  
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
GCGGCTCCGGGCTCTGGAGATGTATTTCTCAATGACACTCTGGCGGTGAGGACAGCCCGT  
CCTTCTCCTTGCTGCAGTGCAGCACACCCCTGGAGAACACCTGGCTCAGGTTGCATCGAGGCTG  
CAAGTCTCTCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT  
AGACAACTTCACTCAGAACCCAGGGATGTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC  
TTCAAGGTCAAGGGGGGCCATGGGCATGCTGGTGCCCTGGCCCGCCGGGACCACTTGCT  
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCTTCGGGACCCCAAGG  
CCCACCGGAGTCAAGGGAGAGGCGGGCTCCAAGGACCCAGGGTGTCTCAGGGAAGCAAG  
GAGCCACTGGCACCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGCGATGGGGTCTCATT  
GGCCCAAAAGGGGAACTGGAACCTAAGGGAGAGAAAGGAGACCTGGGTCTCCAGGAAGCAA  
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTCTGGGGCTCTGGAGCCAGGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCCAACAGGTTTGGCTGGTTTTCTGGAGCTAAAGGAGAT  
CAAGGACAACCTGGACTGCAGGGTGTTCGGGGCTCTGGTGCAGTGGGACACCCAGGTGC  
CAAGGGTGAGCTGGCAGTGTCTGGCTCCCCTGGGCGAGCAGGACTTCAGGGAGCCCCGGGA  
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAGGACAGCAAGGA  
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGAGCCAGG  
GCTGGCAGGTCCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTAGTGTCC  
GTCAGGATTGTGCGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
GACAAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGATGCTGGGTT  
ACTCCAAAGGAAGGGCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT  
GTTCAGTGTCTGGGGCAGCGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA  
TGACTGCAGCCACGAGGAGGACGCAAGGCTGGAGTGCAGCGTCTGACCCGGAACCCCTTCA  
CTTCTCTGCTCCGAGGTGTCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT  
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAAATAAGCTCAACATCATTGA

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## FIGURE 232

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAPHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPFSFSLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD  
GATGSPSGPQGPVVKGEAGLQGPQAGPKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKEG  
KGDGLPGSKGDRGMKGDAGVMGPPGAQGSKGDGFRPGPPGLAGFPAGKGDQGPGLQGVPG  
PPGAVGHPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGTLQGGQGRKGESGVPGPA  
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSEGGQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWGTCIDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLNDNVQCRGTESTLW  
SCTKNSWGHDCSHEEDAGVECSV

### **Transmembrane domain:**

amino acids 47-66 (type II)

### **N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

### **Tyrosine kinase phosphorylation site.**

amino acids 432-440

### **N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

### **Amidation site.**

amino acids 360-364

### **Leucine zipper pattern.**

amino acids 56-78

### **Speract receptor repeat**

amino acids 422-471, 488-519

### **Clq domain proteins.**

amino acids 151-184, 301-334, 316-349

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## FIGURE 233

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGCCCAAACCTACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTCAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTCG  
TGATTCCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCTGATTTC  
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAATTTCTACTTGTCTAAGACAAGTAAATCTGTGTTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAA

0976192.401501

## **FIGURE 234**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758  
<subunit 1 of 1, 98 aa, 1 stop  
<MW: 11081, pI: 6.68, NX(S/T): 1  
MKLMVLVFTIGLTLLLGVSQAMPANRLSCYRKILKDHCHNLPEGVADLTQIDVNVQDHFWDG  
KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

### **Important features:**

#### **Signal peptide:**

amino acids 1-20

#### **N-glycosylation site.**

amino acids 72-76

#### **Tyrosine kinase phosphorylation site.**

amino acids 63-71

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# FIGURE 235

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCAGGTCTGGAGCGAATTCAGCCTGCAGGG  
 CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGCTGGTGGTTGGAGGGC  
 GCGCAGTAGAGCAGCAGCAGCGCGGGTCCCGGAGGCCGGCTCTGCTCGCGCCGAGATG  
 TGGAAATCTCCTTACAGAAACCGACTCGGCTGTGGCCACCGCGCGCCCGCGCTGGCTGTG  
 CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTCTCTCTGGGCTTCTCTTGGGTGGTTTA  
 TAAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT  
 GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACAGACAGATACCACATTGAGC  
 AGGAACAGAACAAACTTTTTCAGCTTGCAGAACAAATTCATCCAGTGGAAAGAAATTTGGCC  
 TGGATTCTGTTGAGCTAGCTCATTATGATGTCTGTGTCTTACCCAAATAAGACTCATCCC  
 AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC  
 ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACTTTTCAGTGTCTTCTCTCTC  
 AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAA  
 TTGGAACGGGACATGAAAATCAATTTGCTCTGGGAAAATTTGTAATTGCCAGATATGGGAAAGT  
 TTTTCAGAGGAAAATAAGGTTAAAAATGCCAGCTGGCAGGGGCCAAAGGAGTCATTCTCTACT  
 CCGACCCCTGCTGACTACTTTTGTCTCTGGGGTGAAGTCTTATCCAGAGCGTTGGAATCTTCTCT  
 GGAGGTGGTGTCCAGCGTGGAAATCTTAAATCTGAATGGTGCAGGAGACCTTCCACACC  
 AGGTTACCCAGCAATGAATATGCTTATAGGCGTGGAAATTCAGAGGCTGTTGGTCTTCCAA  
 GTATTCCTGTTTCATCCAATGGTACTATGATGCACAGAGCTCTTAGAAAAAATGGGTGGC  
 TCAGCACCACAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTCAATGTTGGACCTGG  
 CTTTACTGGAAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTTACCAATGAAGTGA  
 CGAGAATTTACAATGGTATAGGTACTCTCAGAGGAGCAGTGGAAACAGACAGATATGTCATT  
 CTGGGAGGTCAACGGGACTCATGGGTGTTTGGTGGTATTGACCCCTCAGAGTGGAGCAGCTGT  
 TGTTTCATGAAATGTGAGGAGCTTTGGAACTGAAAAAGGAAGGGTGGAGACCTTAGAAGAA  
 CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTCTACTGAGTGGCA  
 GAGGAGAATTCAGACTCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT  
 AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTTGGTACACAACC  
 TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAACTCTTTTATGAAAGTTGG  
 ACTAAAAAAGTCTTCCCCAGAGTTTTCAGTGGCATGCCAGGATTAAGCAAAATTTGGGATCTGG  
 AAATGATTTTGTAGGTGTTCTTCCAACGACTTGAATTTGCTTCAGGCAGAGCAGGTATACTA  
 AAAATTTGGGAAACAAACAAATTCAGCGCTATCCACTGTATCACAGTGTCTATGAAACATAT  
 GAGTTGGTGGAAAAGTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCG  
 AGGAGGATGTGTTTGGAGCTAGCCAATTCATAGTGTCTCCCTTTGATTGTCAGAGATTATG  
 CTGTAGTTTAAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA  
 ATGAAGACATACAGTGTATCATTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT  
 TGCTTCCAAGTTTCAGTGAGAGACTCCAGGACTTGACAAAAGCAACCCAATAGTATTAAGAA  
 TGATGAATGATCAACTCATGTTTCTGGAAGAGCATTATTTGATCCATTAGGGTTACCAGAC  
 AGGCCCTTTTATAGGCATGTCTATGCTCCAAGCAGCCACAACAGTATGCAGGGGAGTC  
 ATTTCCAGGAATTTATGATGCTCTGTTTGTATATTGAAAGCAAAAGTGAGCCCTTCCAGGCCCT  
 GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCCTTCACAGTGCAGGCAGCTGCAGAGACT  
 TTGAGTGAAGTAGCCCTAAGAGGATTTTATAGAAATCCGATTTGAATTTTGTGTGATGTCA  
 CTCAGAAAGAATCGTAATGGGTATATTGATAAAATTTTAAATTTGGTATATTGAAATAAAGT  
 TGAATATTATATATAA

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## FIGURE 236

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756

><subunit 1 of 1, 750 aa, 1 stop

><MW: 84305, pI: 6.93, NX(S/T): 10

MWNLLHETDSAVATARRPRWL CAGALVLAGGFLLGLFGWFIKSSNEATNITPKNHMKAPL  
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH  
PNYISIINEDGNEIFNTSLFEP PPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF  
KLERDMKINCSGKIVIRYGVFRGNKVNAQLAGAKGVILYSDPADYFAPGVKSYPDGWNL  
PGGGVQQRGNILNLNGAGDPLTPGYPAN EYAYRRGIAEAVGLPSIPVHPIGYYDAQKLEKMG  
GSAPPDSSWRGSLKVPYNVGPFGFTGNFSTQKVKMHIHSTNEVTRIYNVIGTLRGAVEPDRYV  
ILGGRD SWVFGIDPQSGAAV VHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW  
AEENSRLQERGVAYINADSSIEGNYTLRV DCTPLMYSLVHNLTKEKSPDEGFEGKSLYES  
WTKKSPSPBFGSMRPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET  
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ  
EMKTYSVSFDLSFSAVKNFTETASKFSERLQDFDKSNPIVLRMMNDQMLFLERAFIDPLGLP  
DRPFYRHHVIYAPSSHNKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE  
TLSEVA

### Signal sequence:

amino acids 1-40

### N-glycosylation sites.

amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642

### Tyrosine kinase phosphorylation sites.

amino acids 363-372, 605-613, 606-613, 617-626

### N-myristoylation sites.

amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713

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